

SEQUENCE LISTING

<110> Kletzien, Rolf F
Reardon, Ilene M
Weiland, Katherine L

<120> HUMAN CASPASE-12 MATERIALS AND METHODS

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<141> 2000-05-09

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<170> PatentIn Ver. 2.0

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Thr Ala Gln Ile Ala Gly Lys Ile Phe Arg Glu His Leu Trp Asn Ser
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aaa aaa cag ctg agt tca gat ata tcc agt gat gga gaa aga gag gcg 288
Lys Lys Gln Leu Ser Ser Asp Ile Ser Ser Asp Gly Glu Arg Glu Ala
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aac atg cct ggc ctc aac atc cgc aac aaa gaa ttc aac tat ctt cat 336
Asn Met Pro Gly Leu Asn Ile Arg Asn Lys Glu Phe Asn Tyr Leu His
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aat cga aat ggt tct gaa ctt gac ctt ttg ggg atg tgagatctac 382
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Lys Phe Val Val Ser Asn Ala Glu Asn Leu Val Asp Asp Ile Thr Glu
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Thr Ala Gln Ile Ala Gly Lys Ile Phe Arg Glu His Leu Trp Asn Ser
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Lys Lys Gln Leu Ser Ser Asp Ile Ser Ser Asp Gly Glu Arg Glu Ala
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aag gct cat gtg gaa aag gac ttc att gct ttc aaa tct tcc aca cca 816
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His Asn Val Ser Trp Arg His Glu Thr Asn Gly Ser Val Phe Ile Ser
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Gln Ile Ile Tyr Tyr Phe Arg Glu Tyr Ser Trp Ser His His Leu Glu
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Glu Ile Phe Gln Lys Val Gln His Ser Phe Glu Thr Pro Asn Ile Leu
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acc cag ctg ccc acc att gaa aga cta tcc atg aca cga tat ttc tat 1008
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Asn Asn Val Leu Asn Thr Asp Glu Ile His Leu Ile Gly Lys Cys Leu
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Lys Phe Val Val Ser Asn Ala Glu Asn Leu Val Asp Asp Ile Thr Glu
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Thr Ala Gln Ile Ala Gly Lys Ile Phe Arg Glu His Leu Trp Asn Ser
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Lys Lys Gln Leu Ser Ser Asp Ile Ser Ser Asp Gly Glu Arg Glu Ala
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ttg ctg atc aag acc ttt cta gat ggc att ttt gat gat ttg atg gaa 96
Leu Leu Ile Lys Thr Phe Leu Asp Gly Ile Phe Asp Asp Leu Met Glu
20 25 30

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Asn Asn Val Leu Asn Thr Asp Glu Ile His Leu Ile Gly Lys Cys Leu
35 40 45

aag ttt gtg gtg agc aat gct gaa aac ctg gtt gat gat atc act gag 192
Lys Phe Val Val Ser Asn Ala Glu Asn Leu Val Asp Asp Ile Thr Glu
50 55 60

aca gct caa att gca ggc aaa ata ttt agg gaa cac ctg tgg aat tcc 240
Thr Ala Gln Ile Ala Gly Lys Ile Phe Arg Glu His Leu Trp Asn Ser
65 70 75 80

aaa aaa cag ctg agt tca gat ata tcc agt gat gga gaa aga gag gcg 288
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85 90 95

aac atg cct ggc ctc aac atc cgc aac aaa gaa ttc aac tat ctt cat 336
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100 105 110

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Asn Arg Asn Gly Ser Glu Leu Asp Leu Leu Gly Met
115 120

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35 40 45
Lys Phe Val Val Ser Asn Ala Glu Asn Leu Val Asp Asp Ile Thr Glu
50 55 60
Thr Ala Gln Ile Ala Gly Lys Ile Phe Arg Glu His Leu Trp Asn Ser
65 70 75 80
Lys Lys Gln Leu Ser Ser Asp Ile Ser Ser Asp Gly Glu Arg Glu Ala
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Leu Leu Ile Lys Thr Phe Leu Asp Gly Ile Phe Asp Asp Leu Met Glu
20 25 30
aat aat gtg tta aat aca gat gag ata cac ctt ata gga aaa tgt cta 144
Asn Asn Val Leu Asn Thr Asp Glu Ile His Leu Ile Gly Lys Cys Leu
35 40 45
aag ttt gtg gtg agc aat gct gaa aac ctg gtt gat gat atc act gag 192
Lys Phe Val Val Ser Asn Ala Glu Asn Leu Val Asp Asp Ile Thr Glu
50 55 60
aca gct caa att gca ggc aaa ata ttt agg gaa cac ctg tgg aat tcc 240
Thr Ala Gln Ile Ala Gly Lys Ile Phe Arg Glu His Leu Trp Asn Ser
65 70 75 80

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cat	tga	aag	act	atc	cat	gac	acg	ata	ttt	cta	tct	ctt	tcc	tgg	gaa	912
His		Lys	Thr	Ile	His	Asp	Thr	Ile	Phe	Leu	Ser	Leu	Ser	Trp	Glu	
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Lys Phe Val Val Ser Asn Ala Glu Asn Leu Val Asp Asp Ile Thr Glu
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Thr Ala Gln Ile Ala Gly Lys Ile Phe Arg Glu His Leu Trp Asn Ser
65 70 75 80
Lys Lys Gln Leu Ser Ser Asp Ile Ser Ser Asp Gly Glu Arg Glu Ala
85 90 95
Asn Met Pro Gly Leu Asn Ile Arg Asn Lys Glu Phe Asn Tyr Leu His
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Glu Asn Leu Gly Tyr Ser Val Val Ile Lys Glu Asn Leu Thr Ala Gln
130 135 140
Glu Met Glu Thr Ala Leu Arg Gln Phe Ala Ala His Pro Glu His Gln
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Ser Ser Asp Ser Thr Phe Leu Val Phe Met Ser His Ser Ile Leu Asn
165 170 175
Gly Ile Cys Gly Thr Lys His Trp Asp Gln Glu Pro Asp Val Leu His
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Lys Asp Lys Pro Lys Val Ile Ile Met Gln Ala Cys Arg Gly Asn Gly
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gatatcactg agacagctca aattgcaggc aaaatattta gggaacacct gtggaattcc 240
aaaaaacagc tgagttcaga tatatccagt gatggagaaa gagaggcgaa catgcctggc 300
ctcaacatcc gcaacaaaga attcaactat cttcataatc gaaatgggttc tgaacttgac 360
cttttgggga tgtgagatct acttgaaaac cttggatact cagtggttat aaaagagaat 420
ctcacagctc agatgggtgct gggattgttt gggtcaccac tgacagtgga aaagccagtg 480

cagataactca tggtcggctc ttgcaaggta acatctgtaa tgatgctgtt acaaaggctc 540
atgtggaaaa ggacttcatt gctttcaaat cttccacacc acgttcaaca ttcatttgag 600
accccaaata tactgaccca gctgcccact attgaaagac tatccatgac acgatatttc 660
tatctctttc ctgggaatta aaaatcgaat tcccgcggcc gccatggcgg ccgggagcat 720
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<210> 12
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<210> 13
<211> 25
<212> DNA
<213> Homo sapiens

<400> 13
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<210> 14
<211> 23
<212> DNA
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<400> 14
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<210> 15
<211> 26
<212> DNA
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<210> 16
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<210> 17
<211> 25
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<400> 18
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<210> 19
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<212> DNA
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<210> 22
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<400> 22
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<210> 23
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<212> DNA
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<400> 23
gtgcttggtc ccacagattc cattcagg 28

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<210> 25
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<212> DNA
<213> Homo sapiens

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<210> 26
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<400> 28
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<210> 29
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<212> DNA
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<400> 29
gtgatatacat caaccaggtt ttcagc 26

<210> 30
<211> 292
<212> DNA
<213> Homo sapiens

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agtagatctc acatccccaa aagggtcaagt tcagaacccat ttogattatg aagatagttg 180
aattctttgt tgcggatgtt gaggccaggc atgttccgcc tctctttctc catcactgga 240
tatatctgca attaatacac acagaatgac tttccccagg acttttctct tt 292

<210> 31
<211> 686
<212> DNA
<213> Homo sapiens

<400> 31
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cagtctgaca tggagtgtca attctaagag gtagtgtaca acgttgagaa gacagaatac 120
ccatgggctt ggtcctatga aacctgcaaa ctctcttcat tccaggactt tcctgggttca 180
tgggtgaaga tgctttctga gacttgaaaa gagtcgtatc tcctctatag cctactttct 240
ttttcagggt cagcaagcat ttgaaagtcc cggaggcaac agtccaaatg cccaccatag 300
aacgagtgtc catgacaaga tatttctacc tctttcctgg caattgaaaa tggttaagca 360
ttgagagttg ttggtggtgt atgaaataaa tgaaagtgtg atattggagg tgagttccga 420
tgaccaatga cagttgagta cttggatggc caaattagtg tactttgttg atgtagtctg 480
gtgattgatt atctggatc ttttattcga ttttttttgc attttgggtt cccccaactc 540
tataattaat caggcaatca atcaatcaag gacgtaagga aaaccaaggc caaatgagat 600
aataaaaaac ccagggtagc acttattaaa atagaaacat actcctgcat ccattactat 660
ttatattcat tacatctcat actcta 686

<210> 32
<211> 533
<212> DNA
<213> Homo sapiens

<400> 32
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aagctttcta ggtgattctt atgcacgtta aaatttggga accactacc tagaatgggg 180
atctaaagtt ctgtccatat ctaagattct atcattttca cagatgagaa accatccaac 240
ggtgttcttg tccacatggg gaagttgctg atcaagacct ttctagatgg catttttgat 300
gatttgatgg aaaataatgt gttaaataca gatgagatac accttatagg aaaatgtcta 360
aagtttgtgg tgagcaatgc tgaaaacctg gttgatgata tcaactgagac agctcaaatt 420
gcaggcaaaa tatttaggga acacctgtgg aattccaaaa aacagctgag ttcagggtgag 480
tattgggggc taacagctag aaattcattc ttattctttc tctactcttc tta 533

<210> 33
<211> 563
<212> DNA
<213> Homo sapiens

<400> 33
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ttttgaaaaa tttcctctag atgatgactc caagaatact ctctgaagta gtagataatt 180
tgggaaatga agacagagcc atttgtttca tgtctccaag aaacattatc tacaaataaa 240
aggcatcaaa atattggagg atgtgatctt ttatacatgt ggaagactcc tggagacata 300

actttgggaa aaaaaatctg attttgtttc tttggagaag agaggggaaac caatgctaaa 360
 taaagatgga cctccaactt ccataaccagg cccagaaaaa gccatcatgg gaccttcctc 420
 actcataaat caccttgatt ttctagtagg ctagaccgaa gtgatatcct ctgggtttgc 480
 aagtagtgga aaagagtgtg agtcctttca gcactaacta cataacagaa aaataataca 540
 gccttgacat tccttgattc tgg 563

<210> 34
 <211> 528
 <212> DNA
 <213> Homo sapiens

<400> 34
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 tgtgcatatg agtatgtgtg tgcatatgtg tatgtgtgtg tgtatgtgta tgtgtgtgta 120
 tttataaata tctcttcttt aatgagacat aatgtctctc ccagatgggtg ctgggattgt 180
 ttggttcacc actgacagtg gaaaagccag tgcagatact catggtcggc tcttgcaagg 240
 taacatctgt aatgatgtg ttacaaaggc tcatgtggaa aaggacttca ttgctttcaa 300
 atcttccaca ccacgtaagt gatttcagag agaataattt ctaaatttct tagtaggttt 360
 ctagatagta ggcttggtg tgatcatatc ttatcaccga acagagcatt tcttctctaa 420
 ttaccaggat attttaggtg gagaaaagat ttaaaatgct gagactttca taattagaaa 480
 gctataaatc ttgatttggg aagaaacggt caaagttaac aggacttt 528

<210> 35
 <211> 555
 <212> DNA
 <213> Homo sapiens

<400> 35
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 aagtatgggg cagaagaaag cccaggcctt gaaacagctc cttcattccc gtgatgtcga 120
 agtgagcccc attccttgga gtcagatagt caaactttgt attgcttata atgagagcca 180
 ggtatttgca gatctttctg tttttttttt tattagattg atctgcagga gatggagatg 240
 aaatgacttt gattacctga gtctcttttc aatctccata tgtttcacaa ttttgttttt 300
 ttaaaacctc gtatagctgc cctcttccct aacctctatc aaaagacact gctttcctct 360
 ctctcaagag cccagagcaa gaaccaggac atatctggat gattagtcaa gaatcttaaa 420
 gaaactagaa taattcctac tccctttctt cttatttttc ttctgcatct actcaaacat 480
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<210> 37
<211> 576
<212> DNA
<213> Homo sapiens
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<210> 38
<211> 611
<212> DNA
<213> Homo sapiens
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cctcgcgcagg cttgcacgat gatgaccttg ggtttgtctt tcagactctg gcagttacgg 120
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ttgttgaaaa tttcaaagta tgggtgtcatc gtgaagaaca tctggctctt gatcccagtg 180
 cttgggtccca cagattccat tcaggatgct atgtgacata aacaccagga atgtgctgtc 240
 tgaggactgg tgctctgggt gagcagcaaa ctgccttagt gctgtttcca tttcctgaaa 300
 gagacccttg agtcactatc gaggaagtct ccatgtgtat gtagtttgta atcaaataat 360
 gggtaggggt caaaaaagg agccagcact aaggaatcag atggttttaga ctgaatagga 420
 ttataagata aacagtgttc tgacataaaa ctagaaaatt tagctgtata gaatattaaa 480
 gttagtaggg tttttatgta gtatcttgcc cagtgggttt tagtaaaacc ttaggtttct 540
 gaagatgctg ggagatggaa taaaatgaag gccaaagtga atgacaatac accaatagga 600
 ccattttgct a 611

<210> 39
 <211> 76
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: peptide

<400> 39
 Arg Glu Lys Ser Trp Gly Lys Ser Phe Cys Val Tyr Leu Gln Ile Tyr
 1 5 10 15
 Pro Val Met Glu Lys Glu Arg Arg Asn Met Pro Gly Leu Asn Ile Arg
 20 25 30
 Asn Lys Glu Arg Asn Tyr Leu His Asn Arg Asn Gly Ser Glu Leu Asp
 35 40 45
 Leu Leu Gly Met Asp Leu Leu Glu Asn Leu Gly Tyr Ser Val Val Ile
 50 55 60
 Lys Glu Asn Leu Thr Ala Gln Val Met Ala Pro Glu
 65 70 75

<210> 40
 <211> 47
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: peptide

<400> 40
 His Leu Pro Thr Phe Phe Phe Arg Phe Ser Lys His Leu Lys Val Pro
 1 5 10 15
 Glu Ala Thr Val Gln Met Pro Thr Ile Glu Arg Val Ser Met Thr Arg
 20 25 30
 Tyr Phe Tyr Leu Phe Pro Gly Asn Lys Trp Leu Ser Ile Glu Ser
 35 40 45

<210> 41

<211> 177
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide

<220>
<221> misc_feature
<222>
<223> Xaa = any amino acid or no amino acid

<400> 41
Val Leu Ala Pro Glu Ala Leu Ala Ser Pro Glu Lys Leu Leu Xaa Met
1 5 10 15
Lys Ile His Gly Pro Ile Leu Thr Tyr Gln Ile Lys Ile Ile Trp Thr
20 25 30
Arg Met Gln Glu Ala Leu Leu Thr Lys Leu Ser Arg Xaa Phe Leu Cys
35 40 45
Thr Leu Lys Phe Gly Asn His Tyr Pro Arg Met Gly Ile Xaa Ser Ser
50 55 60
Val His Ile Xaa Asp Ser Ile Ile Phe Thr Asp Glu Lys Pro Ser Asn
65 70 75 80
Gly Val Leu Val His Met Val Lys Leu Leu Ile Lys Thr Phe Leu Asp
85 90 95
Gly Ile Phe Asp Asp Leu Met Glu Asn Asn Val Leu Asn Thr Asp Glu
100 105 110
Ile His Leu Ile Gly Lys Cys Leu Lys Phe Val Val Ser Asn Ala Glu
115 120 125
Asn Leu Val Asp Asp Ile Thr Glu Thr Ala Gln Ile Ala Gly Lys Ile
130 135 140
Phe Arg Glu His Leu Trp Asn Ser Lys Lys Gln Leu Ser Ser Gly Glu
145 150 155 160
Tyr Trp Gly Leu Thr Ala Arg Asn Ser Phe Leu Phe Phe Leu Tyr Ser
165 170 175

Ser

<210> 42
<211> 99
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide

<220>
<221> misc_feature
<222>
<223> Xaa = any amino acid or no amino acid

<400> 42

Met Ser Pro Gly Val Phe His Met Tyr Lys Arg Ser His Pro Pro Ile
1 5 10 15
Phe Xaa Cys Leu Leu Phe Val Asp Asn Val Ser Trp Arg His Glu Thr
20 25 30
Asn Gly Ser Val Phe Ile Ser Gln Ile Ile Tyr Tyr Phe Arg Glu Tyr
35 40 45
Ser Trp Ser His His Leu Glu Glu Ile Phe Gln Lys Val Gly Ser Ser
50 55 60
Phe Ile Phe Asn Val Met Pro Gln Lys Thr Leu Glu Asn His Leu Xaa
65 70 75 80
Ile Phe Ile Arg Asn Pro Lys Ala Leu Asn Ser Ser Xaa Gln Ser Phe
85 90 95
Leu Thr Pro

<210> 43

<211> 99

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: peptide

<220>

<221> misc_feature

<222>

<223> Xaa = any amino acid or no amino acid

<400> 43

Cys Val Cys Met Cys Met Cys Val Tyr Leu Xaa Ile Ser Leu Leu Xaa
1 5 10 15
Asp Ile Met Ser Leu Pro Asp Gly Ala Gly Ile Val Trp Phe Thr Thr
20 25 30
Asp Ser Gly Lys Ala Ser Ala Asp Thr His Gly Arg Leu Leu Gln Gly
35 40 45
Asn Ile Cys Asn Asp Ala Val Thr Lys Ala His Val Glu Lys Asp Phe
50 55 60
Ile Ala Phe Lys Ser Ser Thr Pro Arg Lys Xaa Phe Gln Arg Glu Xaa
65 70 75 80
Phe Leu Asn Phe Leu Val Gly Phe Xaa Ile Val Gly Leu Ala Met Ile
85 90 95
Ile Ser Tyr

<210> 44

<211> 50

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:peptide

<220>
<221> misc_feature
<222>
<223> Xaa = any amino acid or no amino acid

<400> 44
Ala Leu Ile Ile Ser Asn Thr Lys Phe Asp Tyr Leu Thr Pro Arg Asn
1 5 10 15
Gly Ala His Phe Asp Ile Thr Gly Met Lys Glu Leu Phe Gln Gly Leu
20 25 30
Gly Phe Leu Leu Pro His Thr Xaa Tyr Xaa Met Cys Asp Tyr Met Cys
35 40 45
Asn Xaa
50

<210> 45
<211> 47
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide

<400> 45
Ala Leu Ile Ile Ser Asn Thr Lys Phe Asp Tyr Leu Thr Pro Arg Glu
1 5 10 15
Trp Gly Ser Leu Arg His His Gly Asn Glu Gly Ala Val Ser Arg Pro
20 25 30
Gly Leu Leu Leu Pro His Thr Tyr Met Cys Asp Thr Met Cys Asn
35 40 45

<210> 46
<211> 48
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide

<400> 46
Leu Ser Leu Ala Ile Gln Ser Leu Thr Ile Leu Gln Gly Asn Gly Ala
1 5 10 15
His Phe Asp Ile Thr Gly Met Lys Glu Leu Phe Gln Gly Leu Gly Phe
20 25 30
Phe Cys Pro Ile Leu Asp Ile Arg Cys Val Ile Ile Cys Val Ile Asn
35 40 45

<210> 47
 <211> 51
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: peptide

<400> 47
 Ser Lys Gln Lys Cys Lys Gln Lys Ile Val Lys Val Ile Ala Gln Asp
 1 5 10 15
 Ile Pro Ile Cys Ile Ile Ile Asp Asn Val Ser Arg Arg Asp Ser Thr
 20 25 30
 Arg Gly Ser Ile Phe Ile Thr Gln Ile Leu Ala Cys Phe Gln Arg Tyr
 35 40 45
 Ser Trp Arg
 50

<210> 48
 <211> 89
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: peptide

<400> 48
 Gly Ser Leu Leu Leu Thr Gln Ser Thr Ser Pro Gln Thr Ala His Ser
 1 5 10 15
 Trp Cys Leu Cys His Ile Ala Ser Met Glu Ser Val Gly Pro Ser Thr
 20 25 30
 Gly Ile Lys Ser Gln Met Phe Phe Thr Met Thr Pro Tyr Phe Glu Ile
 35 40 45
 Phe Asn Asn Arg Asn Cys Gln Ser Leu Lys Asp Lys Pro Lys Val Ile
 50 55 60
 Ile Met Gln Ala Cys Arg Gly Ser Glu Ser Pro Ile Arg Lys Leu Ile
 65 70 75 80
 Leu Ile Leu Arg Pro Gln Gly Gly Leu
 85

<210> 49
 <211> 92
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: peptide

<400> 49

Ile Leu Ser Tyr Ser Val Thr Ile Phe Leu Ser Ala Gly Ser Phe Leu
 1 5 10 15
 Thr Leu Pro Ile Ile Leu Gln Thr Thr Tyr Thr Trp Arg Leu Pro Arg
 20 25 30
 Leu Lys Gly Leu Phe Gln Glu Met Glu Thr Ala Leu Arg Gln Phe Ala
 35 40 45
 Ala His Pro Glu His Gln Ser Ser Asp Ser Thr Phe Leu Val Phe Met
 50 55 60
 Ser His Ser Ile Leu Asn Gly Ile Cys Gly Thr Lys His Trp Asp Gln
 65 70 75 80
 Glu Pro Asp Val Leu His Asp Asp Thr Ile Leu Asn
 85 90

<210> 50
 <211> 1026
 <212> DNA
 <213> Homo sapien

<220>
 <221> CDS
 <222> (1)..(372)

<400> 50
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 Met Ala Asp Glu Lys Pro Ser Asn Gly Val Leu Val His Met Val Lys
 1 5 10 15
 ttg ctg atc aag acc ttt cta gat ggc att ttt gat gat ttg atg gaa 96
 Leu Leu Ile Lys Thr Phe Leu Asp Gly Ile Phe Asp Asp Leu Met Glu
 20 25 30
 aat aat gtg tta aat aca gat gag ata cac ctt ata gga aaa tgt cta 144
 Asn Asn Val Leu Asn Thr Asp Glu Ile His Leu Ile Gly Lys Cys Leu
 35 40 45
 aag ttt gtg gtg agc aat gct gaa aac ctg gtt gat gat atc act gag 192
 Lys Phe Val Val Ser Asn Ala Glu Asn Leu Val Asp Asp Ile Thr Glu
 50 55 60
 aca gct caa att gca ggc aaa ata ttt agg gaa cac ctg tgg aat tcc 240
 Thr Ala Gln Ile Ala Gly Lys Ile Phe Arg Glu His Leu Trp Asn Ser
 65 70 75 80
 aaa aaa cag ctg agt tca gat ata tcc agt gat gga gaa aga gag gcg 288
 Lys Lys Gln Leu Ser Ser Asp Ile Ser Ser Asp Gly Glu Arg Glu Ala
 85 90 95
 aac atg cct ggc ctc aac atc cgc aac aaa gaa ttc aac tat ctt cat 336
 Asn Met Pro Gly Leu Asn Ile Arg Asn Lys Glu Phe Asn Tyr Leu His
 100 105 110
 aat cga aat ggt tct gaa ctt gac ctt ttg ggg atg tgagatctac 382
 Asn Arg Asn Gly Ser Glu Leu Asp Leu Leu Gly Met
 115 120
 ttgaaaacct tggataactca gtgggttataa aagagaatct cacagctcag gaaatggaaa 442

cagcactaag gcagtttgct gctcaccag agcaccagtc ctcagacagc acatttctgg 502
 tgtttatgtc acatagcatc ctgaatggaa tctgtgggac caagcactgg gatcaagagc 562
 cagatgttct tcacgatgac accatctttg aaattttcaa caaccgtaac tgccagagtc 622
 tgaaagacaa acccaaggtc atcatcatgc aagcctgccg aggcaatggg gctgggattg 682
 tttgggtcac cactgacagt ggaaaagcca gtgcagatac tcatggtcgg ctcttgcaag 742
 gtaacatctg taatgatgct gttacaaagg ctcattgtga aaaggacttc attgctttca 802
 aatcttccac accacataat gtttcttgga gacatgaaac aaatggctct gtcttcattt 862
 cccaaattat ctactacttc agagagtatt cttggagtca tcatctagag gaaatttttc 922
 aaaaggttca acattcattt gagaccccaa atatactgac ccagctgccc accattgaaa 982
 gactatccat gacacgatat ttctatctct ttcttgggaa ttaa 1026

<210> 51
 <211> 340
 <212> PRT
 <213> Homo sapiens

<400> 51
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 1 5 10 15
 Leu Leu Ile Lys Thr Phe Leu Asp Gly Ile Phe Asp Asp Leu Met Glu
 20 25 30
 Asn Asn Val Leu Asn Thr Asp Glu Ile His Leu Ile Gly Lys Cys Leu
 35 40 45
 Lys Phe Val Val Ser Asn Ala Glu Asn Leu Val Asp Asp Ile Thr Glu
 50 55 60
 Thr Ala Gln Ile Ala Gly Lys Ile Phe Arg Glu His Leu Trp Asn Ser
 65 70 75 80
 Lys Lys Gln Leu Ser Ser Ile Tyr Pro Val Met Glu Lys Glu Arg Arg
 85 90 95
 Thr Cys Leu Ala Leu Asn Ile Arg Asn Lys Glu Phe Asn Tyr Leu His
 100 105 110
 Asn Arg Asn Gly Ser Glu Leu Asp Leu Leu Gly Met Asp Leu Leu Glu
 115 120 125
 Asn Leu Gly Tyr Ser Val Val Ile Lys Glu Asn Leu Thr Ala Gln Glu
 130 135 140
 Met Glu Thr Ala Leu Arg Gln Phe Ala Ala His Pro Glu His Gln Ser
 145 150 155 160
 Ser Asp Ser Thr Phe Leu Val Phe Met Ser His Ser Ile Leu Asn Gly
 165 170 175
 Ile Cys Gly Thr Lys His Trp Asp Gln Glu Pro Asp Val Leu His Asp
 180 185 190

Asp Thr Ile Phe Glu Ile Phe Asn Asn Arg Asn Cys Gln Ser Leu Lys
 195 200 205

Asp Lys Pro Lys Val Ile Ile Met Gln Ala Cys Arg Gly Asn Gly Ala
 210 215 220

Gly Ile Val Trp Phe Thr Thr Asp Ser Gly Lys Ala Ser Ala Asp Thr
 225 230 235 240

His Gly Arg Leu Leu Gln Gly Asn Ile Cys Asn Asp Ala Val Thr Lys
 245 250 255

Ala His Val Glu Lys Asp Phe Ile Ala Phe Lys Ser Ser Thr Pro His
 260 265 270

Asn Val Ser Trp Arg His Glu Thr Asn Gly Ser Val Phe Ile Ser Gln
 275 280 285

Ile Ile Tyr Tyr Phe Arg Glu Tyr Ser Trp Ser His His Leu Glu Glu
 290 295 300

Ile Phe Gln Lys Val Gln His Ser Phe Glu Thr Pro Asn Ile Leu Thr
 305 310 315 320

Gln Leu Pro Thr Ile Glu Arg Leu Ser Met Thr Arg Tyr Phe Tyr Leu
 325 330 335

Phe Pro Gly Asn
 340

<210> 52
 <211> 1001
 <212> DNA
 <213> Homo sapiens

<400> 52
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 atacacctta taggaaaatg tctaaagttt gtgggtgagca atgctgaaaa cctgggtgat 180
 gatatcactg agacagctca aattgcaggc aaaatattta gggaacacct gtggaattcc 240
 aaaaaacagc tgagttcaga tatatccagt gatggagaaa gagaggcgaa catgcctggc 300
 ctcaacatcc gcaacaaaga attcaactat cttcataatc gaaatggttc tgaacttgac 360
 cttttgggga tgtgagatct acttgaaaac cttggatact cagtggttat aaaagagaat 420
 ctcacagctc aggaaatgga aacagcacta aggcagtttg ctgctcacc agagcaccag 480
 tcctcagaca gcacattcct ggtgtttatg tcacatagca tcctgaatgg aatctgtggg 540
 accaagcact gggatcaaga gccagatgtt cttcacgatg acaccatctt tgaaattttc 600
 aacaaccgta actgccagag tctgaaagac aaacccaagg tcatcatcat gcaagcctgc 660
 cgaggcaatg gtgctgggat tgtttggttc accactgaca gtggaaaagc cagtgcagat 720
 actcatggtc ggctcttgca aggtaacatc tgtaatgatg ctgttacaaa ggctcatgtg 780

gaaaaggact tcattgcttt caaatcttcc acaccacgtt caacattcat ttgagacccc 840
 aaatatactg acccagctgc ccaccattga aagactatcc atgacacgat atttctatct 900
 ctttcctggg aattaaaaat cgaattcccg cggccgccat ggcggccggg agcatgcgac 960
 gtcgggccca attcgcccta tagtgagtcg tattacaatt c 1001

<210> 53
 <211> 303
 <212> PRT
 <213> Homo sapiens

<400> 53
 Met Ala Asp Glu Lys Pro Ser Asn Gly Val Leu Val His Met Val Lys
 1 5 10 15
 Leu Leu Ile Lys Thr Phe Leu Asp Gly Ile Phe Asp Asp Leu Met Glu
 20 25 30
 Asn Asn Val Leu Asn Thr Asp Glu Ile His Leu Ile Gly Lys Cys Leu
 35 40 45
 Lys Phe Val Val Ser Asn Ala Glu Asn Leu Val Asp Asp Ile Thr Glu
 50 55 60
 Thr Ala Gln Ile Ala Gly Lys Ile Phe Arg Glu His Leu Trp Asn Ser
 65 70 75 80
 Lys Lys Gln Leu Ser Ser Ile Tyr Pro Val Met Glu Lys Glu Arg Arg
 85 90 95
 Thr Cys Leu Ala Leu Asn Ile Arg Asn Lys Glu Phe Asn Tyr Leu His
 100 105 110
 Asn Arg Asn Gly Ser Glu Leu Asp Leu Leu Gly Met Asp Leu Leu Glu
 115 120 125
 Asn Leu Gly Tyr Ser Val Val Ile Lys Glu Asn Leu Thr Ala Gln Glu
 130 135 140
 Met Glu Thr Ala Leu Arg Gln Phe Ala Ala His Pro Glu His Gln Ser
 145 150 155 160
 Ser Asp Ser Thr Phe Leu Val Phe Met Ser His Ser Ile Leu Asn Gly
 165 170 175
 Ile Cys Gly Thr Lys His Trp Asp Gln Glu Pro Asp Val Leu His Asp
 180 185 190
 Asp Thr Ile Phe Glu Ile Phe Asn Asn Arg Asn Cys Gln Ser Leu Lys
 195 200 205
 Asp Lys Pro Lys Val Ile Ile Met Gln Ala Cys Arg Gly Asn Gly Ala
 210 215 220
 Gly Ile Val Trp Phe Thr Thr Asp Ser Gly Lys Ala Ser Ala Asp Thr
 225 230 235 240
 His Gly Arg Leu Leu Gln Gly Asn Ile Cys Asn Asp Ala Val Thr Lys
 245 250 255

Ala His Val Glu Lys Asp Phe Ile Ala Phe Lys Ser Ser Thr Pro Val
260 265 270
Gln His Ser Phe Glu Thr Pro Asn Ile Leu Thr Gln Leu Pro Thr Ile
275 280 285
Glu Arg Leu Ser Met Thr Arg Tyr Phe Tyr Leu Phe Pro Gly Asn
290 295 300

<210> 54
<211> 874
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222>
<223> n = a or t or g or c

<400> 54
atggctgatg agaaaccatc cnacgggtgtt ctgggtccaca tgggtgaagtt gctgatcaag 60
accttttctag atggcatttt tgatgatttg atggaaaata atgtgttaaa tacagatgag 120
atacacctta taggaaaatg tctaaagttt gtgggtgagca atgctgaaaa cctgggttgat 180
gatatcactg agacagctca aattgcaggc aaaatattta gggaacacct gtggaattcc 240
aaaaaacagc tgagttcaga tatatccagt gatggagaaa gagaggcgaa catgcctggc 300
ctcaacatcc gcaacaaaga attcaactat cttcataatc gaaatgggttc tgaacttgac 360
cttttgggga tgtgagatct acttgaaaac cttggatact cagtggttat aaaagagaat 420
ctcacagctc agatgggtgct gggattgttt ggttcaccac tgacagtgga aaagccagtg 480
cagatactca tggtcggctc ttgcaaggta acatctgtaa tgatgctgtt acaaaggctc 540
atgtggaaaa ggacttcatt gctttcaa atctccacacc acataatgtt tcttgagac 600
atgaaacaaa tggctctgtc ttcatttccc aaattatcta ctacttcaga gagtattctt 660
ggagtcatca tctagaggaa atttttcaaa aggttcaaca ttcatttgag accccaaata 720
tactgaccca gctgccacc attgaaagac tatccatgac acgatatttc tatctctttc 780
ctgggaatta aaaatcgaat tcccgcggcc gccatggcgg ccgggagcat gcgacgtcgg 840
gcccaattcg ccttatagtg agtcgtatta caat 874

<210> 55
<211> 261
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> 8
<223> Xaa = any amino acid or no amino acid

<400> 55
Met Ala Asp Glu Lys Pro Ser Xaa Gly Val Leu Val His Met Val Lys

1	5	10	15
Leu Leu Ile Lys Thr Phe Leu Asp Gly Ile Phe Asp Asp Leu Met Glu	20	25	30
Asn Asn Val Leu Asn Thr Asp Glu Ile His Leu Ile Gly Lys Cys Leu	35	40	45
Lys Phe Val Val Ser Asn Ala Glu Asn Leu Val Asp Asp Ile Thr Glu	50	55	60
Thr Ala Gln Ile Ala Gly Lys Ile Phe Arg Glu His Leu Trp Asn Ser	65	70	75
Lys Lys Gln Leu Ser Ser Ile Tyr Pro Val Met Glu Lys Glu Arg Arg	85	90	95
Thr Cys Leu Ala Leu Asn Ile Arg Asn Lys Glu Phe Asn Tyr Leu His	100	105	110
Asn Arg Asn Gly Ser Glu Leu Asp Leu Leu Gly Met Asp Leu Leu Glu	115	120	125
Asn Leu Gly Tyr Ser Val Val Ile Lys Glu Asn Leu Thr Ala Gln Gly	130	135	140
Ala Gly Ile Val Trp Phe Thr Thr Asp Ser Gly Lys Ala Ser Ala Asp	145	150	155
Thr His Gly Arg Leu Leu Gln Gly Asn Ile Cys Asn Asp Ala Val Thr	165	170	175
Lys Ala His Val Glu Lys Asp Phe Ile Ala Phe Lys Ser Ser Thr Pro	180	185	190
His Asn Val Ser Trp Arg His Glu Thr Asn Gly Ser Val Phe Ile Ser	195	200	205
Gln Ile Ile Tyr Tyr Phe Arg Glu Tyr Ser Trp Ser His His Leu Glu	210	215	220
Glu Ile Phe Gln Lys Val Gln His Ser Phe Glu Thr Pro Asn Ile Leu	225	230	235
Thr Gln Leu Pro Thr Ile Glu Arg Leu Ser Met Thr Arg Tyr Phe Tyr	245	250	255
Leu Phe Pro Gly Asn	260		

<210> 10

<211> 765

<212> DNA

<213> Homo sapiens

<400> 56

atggctgatg agaaaccatc caacgggtgtt ctgggtccaca tgggtgaagtt gctgatcaag 60

acctttctag atggcatttt tgatgatttg atggaaaata atgtgttaaa tacagatgag 120

atacacctta taggaaaatg tctaaagttt gtgggtgagca atgctgaaaa cctgggttgat 180

gatatcactg agacagctca aattgcaggc aaaatattta gggaacacct gtggaattcc 240

aaaaaacagc tgagttcaga tatatccagt gatggagaaa gagaggcgaa catgcctggc 300
 ctcaacatcc gcaacaaaga attcaactat cttcataatc gaaatggttc tgaacttgac 360
 cttttgggga tgtgagatct acttgaaaac cttggatact cagtggttat aaaagagaat 420
 ctcacagctc agatgggtgct gggattgttt gggtcaccac tgacagtggg aaagccagtg 480
 cagatactca tggtcggctc ttgcaaggta acatctgtaa tgatgctgtt acaaaggctc 540
 atgtggaaaa ggacttcatt gctttcaaat cttccacacc acgttcaaca ttcatttgag 600
 accccaaata tactgaccca gctgccact attgaaagac tatccatgac acgatatttc 660
 tatctctttc ctgggaatta aaaatcgaat tcccgcgccc gccatggcgg cggggagcat 720
 gcgacgtcgg gcccaattcg ccctatagtg agtcgtatta caatt 765

<210> 57
 <211> 224
 <212> PRT
 <213> Homo sapien

<400> 57

Met	Ala	Asp	Glu	Lys	Pro	Ser	Asn	Gly	Val	Leu	Val	His	Met	Val	Lys
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Leu	Leu	Ile	Lys	Thr	Phe	Leu	Asp	Gly	Ile	Phe	Asp	Asp	Leu	Met	Glu
			20					25					30		
Asn	Asn	Val	Leu	Asn	Thr	Asp	Glu	Ile	His	Leu	Ile	Gly	Lys	Cys	Leu
			35				40					45			
Lys	Phe	Val	Val	Ser	Asn	Ala	Glu	Asn	Leu	Val	Asp	Asp	Ile	Thr	Glu
	50					55					60				
Thr	Ala	Gln	Ile	Ala	Gly	Lys	Ile	Phe	Arg	Glu	His	Leu	Trp	Asn	Ser
65					70					75				80	
Lys	Lys	Gln	Leu	Ser	Ser	Ile	Tyr	Pro	Val	Met	Glu	Lys	Glu	Arg	Arg
				85					90					95	
Thr	Cys	Leu	Ala	Leu	Asn	Ile	Arg	Asn	Lys	Glu	Phe	Asn	Tyr	Leu	His
		100						105					110		
Asn	Arg	Asn	Gly	Ser	Glu	Leu	Asp	Leu	Leu	Gly	Met	Asp	Leu	Leu	Glu
		115					120					125			
Asn	Leu	Gly	Tyr	Ser	Val	Val	Ile	Lys	Glu	Asn	Leu	Thr	Ala	Gln	Gly
	130					135					140				
Ala	Gly	Ile	Val	Trp	Phe	Thr	Thr	Asp	Ser	Gly	Lys	Ala	Ser	Ala	Asp
145					150					155					160
Thr	His	Gly	Arg	Leu	Leu	Gln	Gly	Asn	Ile	Cys	Asn	Asp	Ala	Val	Thr
				165				170						175	
Lys	Ala	His	Val	Glu	Lys	Asp	Phe	Ile	Ala	Phe	Lys	Ser	Ser	Thr	Pro

180	185	190
Val Gln His Ser Phe Glu Thr Pro Asn Ile Leu Thr Gln Leu Pro Thr		
195	200	205
Ile Glu Arg Leu Ser Met Thr Arg Tyr Phe Tyr Leu Phe Pro Gly Asn		
210	215	220

<210> 58
 <211> 439
 <212> DNA
 <213> Homo sapiens

<400> 58
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 gcagatgaga tatatccagt gatggagaaa gagaggcgaa catgcctggc ctcaacatcc 120
 gcaacaaaga attcaactat cttcataatc gaaatggttc tgaacttgac cttttgggga 180
 tgcgagatct acttgaaaac cttgggatact cagtggttat aaaagagaat ctcacagcta 240
 gcaccttgaa tggaatctgt gggaccaagc actgggatca agagccagat gttcttcacg 300
 atgacaccat ctttgaaatt ttcaacaacc gtaactgcca gagtctgaaa gacaaaccca 360
 aggtcatcat catgcaagcc tgccgaggcg gaatcactag tgaattcgcg gccgcctgca 420
 ggtcgacat atgggagag 439

<210> 59
 <211> 129
 <212> PRT
 <213> Homo sapien

<400> 59
 Pro Ser Gly Lys Leu Lys Leu Cys Pro His Ala His Phe His Glu Leu
 1 5 10 15
 Lys Thr Lys Arg Ala Asp Glu Ile Tyr Pro Val Met Glu Lys Glu Arg
 20 25 30
 Arg Thr Cys Leu Ala Leu Asn Ile Arg Asn Lys Glu Phe Asn Tyr Leu
 35 40 45
 His Asn Arg Asn Gly Ser Glu Leu Asp Leu Leu Gly Met Asp Leu Leu
 50 55 60
 Glu Asn Leu Gly Tyr Ser Val Val Ile Lys Glu Asn Leu Thr Ala Ser
 65 70 75 80
 Ile Leu Asn Gly Ile Cys Gly Thr Lys His Trp Asp Gln Glu Pro Asp
 85 90 95
 Val Leu His Asp Asp Thr Ile Phe Glu Ile Phe Asn Asn Arg Asn Cys
 100 105 110
 Gln Ser Leu Lys Asp Lys Pro Lys Val Ile Ile Met Gln Ala Cys Arg
 115 120 125

Gly

<210> 60
 <211> 477
 <212> DNA
 <213> Homo sapiens

<400> 60
 gcccaaccca gtggcaagtt aaagctttgt cctcatgctc acttccatga actaaagaca 60
 aaaagggcag atgagatata tccagtgatg gagaaagaga ggcgaacatg cctggcctca 120
 acatccgcaa caaagaattc aactatcttc ataatcgaaa tggttctgaa cttgaccttt 180
 tgggggatgtg agatctactt gaaaaccttg gatactcagt gggtataaaa gagagtctca 240
 cagctcagga aatggaaaca gcaactaaggc agtttgctgc tcaccagag caccagtcct 300
 cagacagcac attcctgggtg tttatgtcac atagcatcct gaatggaatc tgtgggacca 360
 agcactggga tcaagagcca gatgttcttc acgatgacac catctttgaa attttcaaca 420
 accgtaactg ccagagtctg aaagacaaac ccaaggtcac catcatgcaa gcctgcc 477

<210> 61
 <211> 158
 <212> PRT
 <213> Homo sapiens

<400> 61
 Ala Gln Pro Ser Gly Lys Leu Lys Leu Cys Pro His Ala His Phe His
 1 5 10 15
 Glu Leu Lys Thr Lys Arg Ala Asp Glu Ile Tyr Pro Val Met Glu Lys
 20 25 30
 Glu Arg Arg Thr Cys Leu Ala Leu Asn Ile Arg Asn Lys Glu Phe Asn
 35 40 45
 Tyr Leu His Asn Arg Asn Gly Ser Glu Leu Asp Leu Leu Gly Met Asp
 50 55 60
 Leu Leu Glu Asn Leu Gly Tyr Ser Val Val Ile Lys Glu Ser Leu Thr
 65 70 75 80
 Ala Gln Glu Met Glu Thr Ala Leu Arg Gln Phe Ala Ala His Pro Glu
 85 90 95
 His Gln Ser Ser Asp Ser Thr Phe Leu Val Phe Met Ser His Ser Ile
 100 105 110
 Leu Asn Gly Ile Cys Gly Thr Lys His Trp Asp Gln Glu Pro Asp Val
 115 120 125
 Leu His Asp Asp Thr Ile Phe Glu Ile Phe Asn Asn Arg Asn Cys Gln
 130 135 140
 Ser Leu Lys Asp Lys Pro Lys Val Ile Ile Met Gln Ala Cys
 145 150 155

<210> 62
 <211> 497
 <212> DNA

<213> Homo sapiens

<400> 62

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gccaaccca gtggcaagtt aaagctttgt cctcatgctc acttccatga actcaagaca      60
aaaagggcag atgagatata tccagtgatg gagaaagaga ggccaacatg cctggcctca      120
acatccgcaa caaagaattc aactatcttc ataatcgaaa tggttctgaa cttgaccttt      180
tgggggatgtg agatctactt gaaaaccttg gatactcagt gggtataaaa gagaatctca      240
cagctcagat ggtgctggga ttgtttggtt caccactgac agtggaaaag ccagtgcaga      300
tactcatggt cggctcttgc aaggtaacat ctgtaatgat gctgttataa aggtcatgt      360
ggaaaaggac ttcattgctt tcaaattctt cacaccacgt tcaacattca tttgagaccc      420
caaataact gaccagctg cccaccattg aaagactatc catgacacga tatttctatc      480
tctttcttgg gaattaa                                     497

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<210> 63

<211> 163

<212> PRT

<213> Homo sapien

<400> 63

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Ala Gln Pro Ser Gly Lys Leu Lys Leu Cys Pro His Ala His Phe His
1          5          10          15
Glu Leu Lys Thr Lys Arg Ala Asp Glu Ile Tyr Pro Val Met Glu Lys
20          25          30
Glu Arg Arg Thr Cys Leu Ala Leu Asn Ile Arg Asn Lys Glu Phe Asn
35          40          45
Tyr Leu His Asn Arg Asn Gly Ser Glu Leu Asp Leu Leu Gly Met Asp
50          55          60
Leu Leu Glu Asn Leu Gly Tyr Ser Val Val Ile Lys Glu Asn Leu Thr
65          70          75          80
Ala Gln Gly Ala Gly Ile Val Trp Phe Thr Thr Asp Ser Gly Lys Ala
85          90          95
Ser Ala Asp Thr His Gly Arg Leu Leu Gln Gly Asn Ile Cys Asn Asp
100         105         110
Ala Val Thr Lys Ala His Val Glu Lys Asp Phe Ile Ala Phe Lys Ser
115         120         125
Ser Thr Pro Val Gln His Ser Phe Glu Thr Pro Asn Ile Leu Thr Gln
130         135         140
Leu Pro Thr Ile Glu Arg Leu Ser Met Thr Arg Tyr Phe Tyr Leu Phe
145         150         155         160
Pro Gly Asn

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<210> 64
 <211> 661
 <212> DNA
 <213> Homo sapiens

<400> 64
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 aaaagggcag atgagatata tccagtgatg gagaaagaga gggaacatg cctggcctca 120
 acatccgcaa caaagaattc aactatcttc ataatcgaaa tggttctgaa cttgaccttt 180
 aggggatgtg agatctactt gaaaaccttg gatactcagt gggtataaaa gagaatctca 240
 cagctcagat ggtgctggga ttgtttggtt caccactgac agtggaaaag ccagtgcaga 300
 tactcatggt cggtcttgc aaggtaacat ctgtaatgat gctgttaca aggctcatgt 360
 ggaaaaggac ttcatgtgtt tcaaatcttc cacaccacat aatgtttctt ggagacatga 420
 aacaaatggc tctgtcttca tttccaaat tatctactac ttcagagagt attcttggag 480
 tcatcatcta gaggaaatct ttcaaaaggt tcaacattca tttgagaccc caaatatact 540
 gaccagctg cccaccattg aaagactatc catgacacga tatttctatc tctttcctgg 600
 gaattaaaaa tcgaattccc gcggccgcca tggcgccgg gagcatgcga cgtcggggccc 660
 a 661

<210> 65
 <211> 200
 <212> PRT
 <213> Homo sapiens

<400> 65
 Ala Gln Pro Ser Gly Lys Leu Lys Leu Cys Pro His Ala His Phe His
 1 5 10 15
 Glu Leu Lys Thr Lys Arg Ala Asp Glu Ile Tyr Pro Val Met Glu Lys
 20 25 30
 Glu Arg Arg Thr Cys Leu Ala Leu Asn Ile Arg Asn Lys Glu Phe Asn
 35 40 45
 Tyr Leu His Asn Arg Asn Gly Ser Glu Leu Asp Leu Leu Gly Met Asp
 50 55 60
 Leu Leu Glu Asn Leu Gly Tyr Ser Val Val Ile Lys Glu Asn Leu Thr
 65 70 75 80
 Ala Gln Gly Ala Gly Ile Val Trp Phe Thr Thr Asp Ser Gly Lys Ala
 85 90 95
 Ser Ala Asp Thr His Gly Arg Leu Leu Gln Gly Asn Ile Cys Asn Asp
 100 105 110
 Ala Val Thr Lys Ala His Val Glu Lys Asp Phe Ile Ala Phe Lys Ser
 115 120 125

Ser Thr Pro His Asn Val Ser Trp Arg His Glu Thr Asn Gly Ser Val
 130 135 140
 Phe Ile Ser Gln Ile Ile Tyr Tyr Phe Arg Glu Tyr Ser Trp Ser His
 145 150 155 160
 His Leu Glu Glu Ile Phe Gln Lys Val Gln His Ser Phe Glu Thr Pro
 165 170 175
 Asn Ile Leu Thr Gln Leu Pro Thr Ile Glu Arg Leu Ser Met Thr Arg
 180 185 190
 Tyr Phe Tyr Leu Phe Pro Gly Asn
 195 200

<210> 66
 <211> 758
 <212> DNA
 <213> Homo sapiens

<400> 66
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 aaaagggcag atgagatata tccagtgatg gagaaagaga ggcgaacatg cctggcctca 120
 acatccgcaa caaagaattc aactatcttc ataatcgaaa tggttctgaa cttgaccttt 180
 tgggggatgtg agatctactt gaaaaccttg gatactcagt gggtataaaa gagaatctca 240
 cagctcagga aatggaaaca gcactaaggc agtttgctgc tcaccagag caccagtcct 300
 cagacagcac attcctggcg tttatgtcac atagcctcct gaatagaatc tgtgggacca 360
 agcactggga tcaagagcca gatgttcttc acgatgacac catctttgaa attttcaaca 420
 accgtaactg ccagagtctg aaagacaaac ccaagatggg gctgggattg tttggttcac 480
 cactgacagt ggaaaaagcc agtgcagata ctcatggctg gctcttgcaa ggtaacatct 540
 gtaatgatgc tgttacaaag gttcatgtgg aaaaggactt cattgctttc aaatcttcca 600
 caccacgttc aacattcatt tgagacccca aatatactga ccagctgcc caccattgaa 660
 agactatcca tgacacgata tttctatctc tttcttgagg attaaaaatc gaattcccgc 720
 ggccgccagg cggccgggag catgcgacgt cgggccca 758

<210> 67
 <211> 232
 <212> PRT
 <213> Homo sapien

<400> 67
 Ala Gln Pro Ser Gly Lys Leu Lys Leu Cys Pro His Ala His Phe His
 1 5 10 15
 Glu Leu Lys Thr Lys Arg Ala Asp Glu Ile Tyr Pro Val Met Glu Lys
 20 25 30
 Glu Arg Arg Thr Cys Leu Ala Leu Asn Ile Arg Asn Lys Glu Phe Asn
 35 40 45

Tyr Leu His Asn Arg Asn Gly Ser Glu Leu Asp Leu Leu Gly Met Asp
50 55 60

Leu Leu Glu Asn Leu Gly Tyr Ser Val Val Ile Lys Glu Asn Leu Thr
65 70 75 80

Ala Gln Glu Met Glu Thr Ala Leu Arg Gln Phe Ala Ala His Pro Glu
85 90 95

His Gln Ser Ser Asp Ser Thr Phe Leu Ala Phe Met Ser His Ser Ile
100 105 110

Leu Asn Arg Ile Cys Gly Thr Lys His Trp Asp Gln Glu Pro Asp Val
115 120 125

Leu His Asp Asp Thr Ile Phe Glu Ile Phe Asn Asn Arg Asn Cys Gln
130 135 140

Ser Leu Lys Asp Lys Pro Lys Gly Ala Gly Ile Val Trp Phe Thr Thr
145 150 155 160

Asp Val Glu Lys Ala Ser Ala Asp Thr His Gly Arg Leu Leu Gln Gly
165 170 175

Asn Ile Cys Asn Asp Ala Val Thr Lys Val His Val Glu Lys Asp Phe
180 185 190

Ile Ala Phe Lys Ser Ser Thr Pro Val Gln His Ser Phe Glu Thr Pro
195 200 205

Asn Ile Leu Thr Gln Leu Pro Thr Ile Glu Arg Leu Ser Met Thr Arg
210 215 220

Tyr Phe Tyr Leu Phe Pro Gly Asn
225 230

<210> 68
<211> 503
<212> DNA
<213> Homo sapiens

<400> 68
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acctttctag atggcatttt tgatgatttg atggaaaata atgtgttaaa tacagatgag 120
atacacctta taggaaaatg tctaaagttt gtggtgagca atgctgaaaa cctggttgat 180
gatatcactg agacagctca gattgcaggc aaaatattta gggaacacct gtggaattcc 240
aaaaaacagc tgagttcaga tatatccagt gatggagaaa gagaggcgaa catgcctggc 300
ctcaacatcc gcaacaaaga attcaactat cttcataatc gaaatggttc tgaacttgac 360
cttttgggga tgtgagatct acttgaaaac cttggatact cagtggttat aaaagagaat 420
ctcacagctc aggaaatgga aacagcacat tcttgggtgtt tatgtcacat agcatcctga 480
atggaatctg tgggaccaag cac 503

<210> 69
 <211> 166
 <212> PRT
 <213> Homo sapien

<400> 69
 Met Ala Asp Glu Lys Pro Ser Asn Gly Val Leu Val His Met Val Lys
 1 5 10 15
 Leu Leu Ile Lys Thr Phe Leu Asp Gly Ile Phe Asp Asp Leu Met Glu
 20 25 30
 Asn Asn Val Leu Asn Thr Asp Glu Ile His Leu Ile Gly Lys Cys Leu
 35 40 45
 Lys Phe Val Val Ser Asn Ala Glu Asn Leu Val Asp Asp Ile Thr Glu
 50 55 60
 Thr Ala Gln Ile Ala Gly Lys Ile Phe Arg Glu His Leu Trp Asn Ser
 65 70 75 80
 Lys Lys Gln Leu Ser Ser Ile Tyr Pro Val Met Glu Lys Glu Arg Arg
 85 90 95
 Thr Cys Leu Ala Leu Asn Ile Arg Asn Lys Glu Phe Asn Tyr Leu His
 100 105 110
 Asn Arg Asn Gly Ser Glu Leu Asp Leu Leu Gly Met Asp Leu Leu Glu
 115 120 125
 Asn Leu Gly Tyr Ser Val Val Ile Lys Glu Asn Leu Thr Ala Gln Glu
 130 135 140
 Met Glu Ser Thr Phe Leu Val Phe Met Ser His Ser Ile Leu Asn Gly
 145 150 155 160
 Ile Cys Gly Thr Lys His
 165

<210> 70
 <211> 1129
 <212> DNA
 <213> Homo sapiens

<400> 70
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 tgatcaagac ctttctagat ggcatttttg atgatttgat ggaaaataat gtgttaaata 120
 cagatgagat acaccttata ggaaaatgtc taaagtttgt ggtgagcaat gctgaaaacc 180
 tggttgatga tatcactgag acagctcaaa ttgcaggcaa aatatttagg gaacacctgt 240
 ggaattccaa aaaacagctg agttcagctc ttctggaaat ccagggtgcc caaccacgtg 300
 gcaagttaaa gctttgtcct catgctcact tccatgaact aaagacaaaa agggcagatg 360
 agatatatcc agtgatggag aaagagaggc gaacatgcct ggcctcaaca tccgcaacaa 420
 agaattcaac tatcttcata atcgaaatgg ttctgaactt gaccttttgg ggatgtgaga 480

tctacttgaa aaccttggat actcagtggg tataaaagag aatctcacag ctccaggaaat 540
 ggaaacagca ctaaggcagt ttgctgctca cccagagcac cagtcctcag acagcacatt 600
 cctgggtgttt atgtcacata gcacccctgaa tggaatctgt gggaccaagc actgggatca 660
 agagccagat gttcttcacg atgacaccat ctttgaaatt ttcaacaacc gtaactgcca 720
 gagtctgaaa gacaaaccca aggtcatcat catgcaagcc tgccgaggca atgggtgctgg 780
 gattgtttgg ttcaccactg acagtggaaa agccagtgcg gatactcatg gtcgggtctt 840
 gcaaggtaac atctgtaatg atgctgttac aaaggctcat gtggaaaagg acttcattgc 900
 tttcaaatct tccacaccac ataatgtttc ttggagacat gaaacaaatg gctctgtctt 960
 catttcccaa attatctact acttcagaga gtattcttgg agtcatcatc tagaggaaat 1020
 ttttcaaaag gttcaacatt catttgagac cccaaatata ctgaccacgc tgcccacat 1080
 tgaaagacta tccatgacac gatatttcta tctctttcct gggaattaa 1129

<210> 71
 <211> 372
 <212> PRT
 <213> Homo sapiens

<400> 71
 Met Ala Asp Glu Lys Pro Ser Asn Gly Val Leu Val His Met Val Lys
 1 5 10 15
 Leu Leu Ile Lys Thr Phe Leu Asp Gly Ile Phe Asp Asp Leu Met Glu
 20 25 30
 Asn Asn Val Leu Asn Thr Asp Glu Ile His Leu Ile Gly Lys Cys Leu
 35 40 45
 Lys Phe Val Val Ser Asn Ala Glu Asn Leu Val Asp Asp Ile Thr Glu
 50 55 60
 Thr Ala Gln Ile Ala Gly Lys Ile Phe Arg Glu His Leu Trp Asn Ser
 65 70 75 80
 Lys Lys Gln Leu Ser Ser Ala Leu Leu Glu Ile Gln Gly Ala Gln Pro
 85 90 95
 Ser Gly Lys Leu Lys Leu Cys Pro His Ala His Phe His Glu Leu Lys
 100 105 110
 Thr Lys Arg Ala Asp Glu Ile Tyr Pro Val Met Glu Lys Glu Arg Arg
 115 120 125
 Thr Cys Leu Ala Leu Asn Ile Arg Asn Lys Glu Phe Asn Tyr Leu His
 130 135 140
 Asn Arg Asn Gly Ser Glu Leu Asp Leu Leu Gly Met Asp Leu Leu Glu
 145 150 155 160
 Asn Leu Gly Tyr Ser Val Val Ile Lys Glu Asn Leu Thr Ala Gln Glu
 165 170 175

Met Glu Thr Ala Leu Arg Gln Phe Ala Ala His Pro Glu His Gln Ser
180 185 190

Ser Asp Ser Thr Phe Leu Val Phe Met Ser His Ser Ile Leu Asn Gly
195 200 205

Ile Cys Gly Thr Lys His Trp Asp Gln Glu Pro Asp Val Leu His Asp
210 215 220

Asp Thr Ile Phe Glu Ile Phe Asn Asn Arg Asn Cys Gln Ser Leu Lys
225 230 235 240

Asp Lys Pro Lys Val Ile Ile Met Gln Ala Cys Arg Gly Asn Gly Ala
245 250 255

Gly Ile Val Trp Phe Thr Thr Asp Ser Gly Lys Ala Ser Ala Asp Thr
260 265 270

His Gly Arg Leu Leu Gln Gly Asn Ile Cys Asn Asp Ala Val Thr Lys
275 280 285

Ala His Val Glu Lys Asp Phe Ile Ala Phe Lys Ser Ser Thr Pro His
290 295 300

Asn Val Ser Trp Arg His Glu Thr Asn Gly Ser Val Phe Ile Ser Gln
305 310 315 320

Ile Ile Tyr Tyr Phe Arg Glu Tyr Ser Trp Ser His His Leu Glu Glu
325 330 335

Ile Phe Gln Lys Val Gln His Ser Phe Glu Thr Pro Asn Ile Leu Thr
340 345 350

Gln Leu Pro Thr Ile Glu Arg Leu Ser Met Thr Arg Tyr Phe Tyr Leu
355 360 365

Phe Pro Gly Asn
370

<210> 72
<211> 1130
<212> DNA
<213> Homo sapiens

<400> 72
tgattgccat ggctgatgag aaaccatcca acggtgttct ggtccacatg gtgaagttgc 60
tgatcaagac ctttctagat ggcatTTTTg atgatttgat ggaaaataat gtgttaaata 120
cagatgagat acaccttata ggaaaatgtc taaagtttgt ggtgagcaat gctgaaaacc 180
tggttgatga tatcactgag acagctcaaa ttgcaggcaa aatatttagg gaacacctgt 240
ggaattccaa aaaacagctg agttcagctc ttctggaaat ccagggtgcc caaccctagt 300
gcaagttaaa gctttgtcct catgctcact tccatgaact aaagacaaaa agggcagatg 360
agatatatcc agtgatggag aaagagaggc gaacatgcct ggccctcaac atccgcaaca 420
aagaattcaa ctatcttcat aatcgaaatg gttctgaact tgaccttttg gggatgcgag 480
atctacttga aaaccttgga tactcagtgg ttataaaaga gaatctcaca gctcaggaaa 540

tggaaacagc actaaggcag tttgctgctc acccagagca ccagtcctca gacagcacat 600
 tcctgggtgtt tatgtcacat agcatcctga atggaatctg tgggaccaag cactgggatac 660
 aagagccaga tgttcttcac gatgacacca tctttgaaat tttcaacaac cgtaactgcc 720
 agagtctgaa agacaaaccc aaggtcatca tcatgcaagc ctgccgaggc aatgggtgctg 780
 ggattgtttg gttcaccact gacagtggaa aagccagtgc agatactcat ggtcggctct 840
 tgcaaggtaa catctgtaat gatgctgtta caaaggctca tgtggaaaag gacttcattg 900
 ctttcaaatac ttccacacca cataatgttt cttggagaca tgaaacaaat ggctctgtct 960
 tcatttccca aattatctac tacttcagag agtattcttg gagtcacatc cttagaggaaa 1020
 tttttcaaaa ggttcaacat tcatttgaga ccccaaatat actgacccag ctgcccacca 1080
 ttgaaagact atccatgaca cgatatttct atctctttcc tgggaattaa 1130

<210> 73
 <211> 373
 <212> PRT
 <213> Homo sapiens

<400> 73

Met Ala Asp Glu Lys Pro Ser Asn Gly Val Leu Val His Met Val Lys
 1 5 10 15
 Leu Leu Ile Lys Thr Phe Leu Asp Gly Ile Phe Asp Asp Leu Met Glu
 20 25 30
 Asn Asn Val Leu Asn Thr Asp Glu Ile His Leu Ile Gly Lys Cys Leu
 35 40 45
 Lys Phe Val Val Ser Asn Ala Glu Asn Leu Val Asp Asp Ile Thr Glu
 50 55 60
 Thr Ala Gln Ile Ala Gly Lys Ile Phe Arg Glu His Leu Trp Asn Ser
 65 70 75 80
 Lys Lys Gln Leu Ser Ser Ala Leu Leu Glu Ile Gln Gly Ala Gln Pro
 85 90 95
 Ser Gly Lys Leu Lys Leu Cys Pro His Ala His Phe His Glu Leu Lys
 100 105 110
 Thr Lys Arg Ala Asp Glu Ile Tyr Pro Val Met Glu Lys Glu Arg Arg
 115 120 125
 Thr Cys Leu Ala Leu Asn Ile Arg Asn Lys Glu Phe Asn Tyr Leu His
 130 135 140
 Asn Arg Asn Gly Ser Glu Leu Asp Leu Leu Gly Met Arg Asp Leu Leu
 145 150 155 160
 Glu Asn Leu Gly Tyr Ser Val Val Ile Lys Glu Asn Leu Thr Ala Gln
 165 170 175
 Glu Met Glu Thr Ala Leu Arg Gln Phe Ala Ala His Pro Glu His Gln

180										185					190				
Ser	Ser	Asp	Ser	Thr	Phe	Leu	Val	Phe	Met	Ser	His	Ser	Ile	Leu	Asn				
		195					200						205						
Gly	Ile	Cys	Gly	Thr	Lys	His	Trp	Asp	Gln	Glu	Pro	Asp	Val	Leu	His				
	210					215					220								
Asp	Asp	Thr	Ile	Phe	Glu	Ile	Phe	Asn	Asn	Arg	Asn	Cys	Gln	Ser	Leu				
225					230					235					240				
Lys	Asp	Lys	Pro	Lys	Val	Ile	Ile	Met	Gln	Ala	Cys	Arg	Gly	Asn	Gly				
				245					250					255					
Ala	Gly	Ile	Val	Trp	Phe	Thr	Thr	Asp	Ser	Gly	Lys	Ala	Ser	Ala	Asp				
			260					265					270						
Thr	His	Gly	Arg	Leu	Leu	Gln	Gly	Asn	Ile	Cys	Asn	Asp	Ala	Val	Thr				
		275					280					285							
Lys	Ala	His	Val	Glu	Lys	Asp	Phe	Ile	Ala	Phe	Lys	Ser	Ser	Thr	Pro				
	290					295					300								
His	Asn	Val	Ser	Trp	Arg	His	Glu	Thr	Asn	Gly	Ser	Val	Phe	Ile	Ser				
305					310					315					320				
Gln	Ile	Ile	Tyr	Tyr	Phe	Arg	Glu	Tyr	Ser	Trp	Ser	His	His	Leu	Glu				
				325					330					335					
Glu	Ile	Phe	Gln	Lys	Val	Gln	His	Ser	Phe	Glu	Thr	Pro	Asn	Ile	Leu				
			340					345					350						
Thr	Gln	Leu	Pro	Thr	Ile	Glu	Arg	Leu	Ser	Met	Thr	Arg	Tyr	Phe	Tyr				
		355					360					365							
Leu	Phe	Pro	Gly	Asn															
		370																	

<210> 74
 <211> 867
 <212> DNA
 <213> Homo sapiens

<400> 74
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 gctcacttcc atgaactaaa gacaaaaagg gcagatgaga tatatccagt gatggagaaa 120
 gagaggcgaa catgcctggc cctcaacatc cgcaacaaag aattcaacta tcttcataat 180
 cgaaatgggt ctgaacttga ccttttgggg atgcgagatc tacttgaaaa ccttggatac 240
 tcagtgggta taaaagagaa totcacagct caggaaatgg aaacagcact aaggcagttt 300
 gctgctcacc cagagcacca gtcctcagac agcacattcc tgggtgtttat gtcacatagc 360
 atcctgaatg gaatctgtgg gaccaagcac tgggatcaag agccagatgt tcttcacgat 420
 gacaccatct ttgaaatttt caacaaccgt aactgccaga gtctgaaaga caaacccaag 480
 gtcacatca tgcaagcctg ccgaggcaat ggtgctggga ttgtttgggt caccactgac 540

agtggaaaag ccagtgcaga tactcatggt cggctcttgc aaggtaacat ctgtaatgat 600
gctgttacaa aggctcatgt ggaaaaggac ttcattgctt tcaaattctt cacaccacat 660
aatgtttctt ggagacatga aacaaatggc tctgtcttca tttcccaa at tctactac 720
ttcagagagt attcttggag tcatcatcta gaggaattt ttcaaaagg tcaacattca 780
tttgagaccc caaatatact gaccagctg cccaccattg aaagactatc catgacacga 840
tatttctatc tctttcttgg gaattaa 867

<210> 75
<211> 288
<212> PRT
<213> Homo sapiens

<400> 75
Ser Ala Leu Leu Glu Ile Gln Gly Ala Gln Pro Ser Gly Lys Leu Lys
1 5 10 15
Leu Cys Pro His Ala His Phe His Glu Leu Lys Thr Lys Arg Ala Asp
20 25 30
Glu Ile Tyr Pro Val Met Glu Lys Glu Arg Arg Thr Cys Leu Ala Leu
35 40 45
Asn Ile Arg Asn Lys Glu Phe Asn Tyr Leu His Asn Arg Asn Gly Ser
50 55 60
Glu Leu Asp Leu Leu Gly Met Arg Asp Leu Leu Glu Asn Leu Gly Tyr
65 70 75 80
Ser Val Val Ile Lys Glu Asn Leu Thr Ala Gln Glu Met Glu Thr Ala
85 90 95
Leu Arg Gln Phe Ala Ala His Pro Glu His Gln Ser Ser Asp Ser Thr
100 105 110
Phe Leu Val Phe Met Ser His Ser Ile Leu Asn Gly Ile Cys Gly Thr
115 120 125
Lys His Trp Asp Gln Glu Pro Asp Val Leu His Asp Asp Thr Ile Phe
130 135 140
Glu Ile Phe Asn Asn Arg Asn Cys Gln Ser Leu Lys Asp Lys Pro Lys
145 150 155 160
Val Ile Ile Met Gln Ala Cys Arg Gly Asn Gly Ala Gly Ile Val Trp
165 170 175
Phe Thr Thr Asp Ser Gly Lys Ala Ser Ala Asp Thr His Gly Arg Leu
180 185 190
Leu Gln Gly Asn Ile Cys Asn Asp Ala Val Thr Lys Ala His Val Glu
195 200 205
Lys Asp Phe Ile Ala Phe Lys Ser Ser Thr Pro His Asn Val Ser Trp
210 215 220
Arg His Glu Thr Asn Gly Ser Val Phe Ile Ser Gln Ile Ile Tyr Tyr

225		230		235		240
Phe Arg Glu Tyr Ser Trp Ser His His Leu Glu Glu Ile Phe Gln Lys						
	245			250		255
Val Gln His Ser Phe Glu Thr Pro Asn Ile Leu Thr Gln Leu Pro Thr						
	260		265		270	
Ile Glu Arg Leu Ser Met Thr Arg Tyr Phe Tyr Leu Phe Pro Gly Asn						
	275	280		285		

<210> 76
 <211> 1130
 <212> DNA
 <213> Homo sapiens

<400> 76
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 tgatcaagac ctttctagat ggcatttttg atgatttgat ggaaaataat gtgttaaata 120
 cagatgagat acaccttata ggaaaatgtc taaagtttgt ggtgagcaat gctgaaaacc 180
 tggttgatga tctactgag acagctcaaa ttgcaggcaa aatatttagg gaacacctgt 240
 ggaattccaa aaaacagctg agttcagctc ttctggaaat ccagggtgcc caaccctagt 300
 gcaagttaaa gctttgtcct catgctcact tccatgaact aaagacaaaa agggcagatg 360
 agatatatcc agtgatggag aaagagagggc gaacatgcct ggccctcaac atccgcaaca 420
 aagaattcaa ctatcttcac aatcgaaatg gttctgaact tgaccttttg gggatgcgag 480
 atctacttga aaaccttgga tactcagtgg ttataaaaaga gaatctcaca gctcaggaaa 540
 tggaaacagc actaaggcag tttgctgctc acccagagca ccagtcctca gacagcacat 600
 tcttggtgtt tatgtcacat ggcacctga atggaatctg tgggaccaag cactgggac 660
 aagagccaga tgttcttcac gatgacacca tctttgaaat tttcaacaac cgtaactgcc 720
 agagtctgaa agacaaaccc aaggctcatca tcatgcaagc ctgdcgaggc aatggtgctg 780
 ggattgtttg gttcaccact gacagtggaa aagcagtgac agatactcat ggtcggctct 840
 tgcaaggtaa catctgtaat gatgctgtta caaaggctca tgtggaaaag gacttcattg 900
 ctttcaaata tccacacca cataatgttt cttggagaca tgaaacaaat ggctctgtct 960
 tcatttccca aattatctac tacttcagag agtattcttg gagtcatcat ctagaggaaa 1020
 tttttcaaaa ggttcaacat tcatttgaga ccccaaatat actgaccag ctgcccacca 1080
 ttgaaagact atccatgaca cgatatttct atctctttcc tgggaattaa 1130

<210> 77
 <211> 373
 <212> PRT
 <213> Homo sapiens

<400> 77
 Met Ala Asp Glu Lys Pro Ser Asn Gly Val Leu Val His Met Val Lys

1													5													10													15
Leu	Leu	Ile	Lys 20	Thr	Phe	Leu	Asp	Gly 25	Ile	Phe	Asp	Asp	Leu	Met	Glu																								
Asn	Asn	Val 35	Leu	Asn	Thr	Asp	Glu 40	Ile	His	Leu	Ile	Gly 45	Lys	Cys	Leu																								
Lys	Phe 50	Val	Val	Ser	Asn	Ala 55	Glu	Asn	Leu	Val	Asp 60	Asp	Ile	Thr	Glu																								
Thr 65	Ala	Gln	Ile	Ala	Gly 70	Lys	Ile	Phe	Arg	Glu 75	His	Leu	Trp	Asn	Ser 80																								
Lys	Lys	Gln	Leu	Ser 85	Ser	Ala	Leu	Leu	Glu 90	Ile	Gln	Gly	Ala	Gln	Pro 95																								
Ser	Gly	Lys	Leu 100	Lys	Leu	Cys	Pro	His 105	Ala	His	Phe	His	Glu	Leu	Lys																								
Thr	Lys	Arg 115	Ala	Asp	Glu	Ile	Tyr 120	Pro	Val	Met	Glu	Lys 125	Glu	Arg	Arg																								
Thr	Cys 130	Leu	Ala	Leu	Asn	Ile 135	Arg	Asn	Lys	Glu	Phe 140	Asn	Tyr	Leu	His																								
Asn 145	Arg	Asn	Gly	Ser	Glu 150	Leu	Asp	Leu	Leu	Gly 155	Met	Arg	Asp	Leu	Leu 160																								
Glu	Asn	Leu	Gly	Tyr 165	Ser	Val	Val	Ile	Lys 170	Glu	Asn	Leu	Thr	Ala 175	Gln																								
Glu	Met	Glu	Thr 180	Ala	Leu	Arg	Gln	Phe 185	Ala	Ala	His	Pro	Glu 190	His	Gln																								
Ser	Ser	Asp 195	Ser	Thr	Phe	Leu	Val 200	Phe	Met	Ser	His	Gly 205	Ile	Leu	Asn																								
Gly	Ile 210	Cys	Gly	Thr	Lys	His 215	Trp	Asp	Gln	Glu	Pro 220	Asp	Val	Leu	His																								
Asp 225	Asp	Thr	Ile	Phe	Glu 230	Ile	Phe	Asn	Asn	Arg 235	Asn	Cys	Gln	Ser	Leu 240																								
Lys	Asp	Lys	Pro	Lys 245	Val	Ile	Ile	Met	Gln 250	Ala	Cys	Arg	Gly	Asn 255	Gly																								
Ala	Gly	Ile	Val 260	Trp	Phe	Thr	Thr	Asp 265	Ser	Gly	Lys	Ala	Ser 270	Ala	Asp																								
Thr	His	Gly 275	Arg	Leu	Leu	Gln	Gly 280	Asn	Ile	Cys	Asn	Asp 285	Ala	Val	Thr																								
Lys	Ala 290	His	Val	Glu	Lys	Asp 295	Phe	Ile	Ala	Phe	Lys 300	Ser	Ser	Thr	Pro																								
His 305	Asn	Val	Ser	Trp	Arg 310	His	Glu	Thr	Asn	Gly 315	Ser	Val	Phe	Ile	Ser 320																								
Gln	Ile	Ile	Tyr	Tyr	Phe	Arg	Glu	Tyr	Ser	Trp	Ser	His	His	Leu	Glu																								

325	330	335
Glu Ile Phe Gln Lys Val Gln His Ser Phe Glu Thr Pro Asn Ile Leu		
340	345	350
Thr Gln Leu Pro Thr Ile Glu Arg Leu Ser Met Thr Arg Tyr Phe Tyr		
355	360	365
Leu Phe Pro Gly Asn		
370		

<210> 78
 <211> 867
 <212> DNA
 <213> Homo sapiens

<400> 78
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 gctcacttcc atgaactaaa gacaaaaagg gcagatgaga tatatccagt gatggagaaa 120
 gagaggcgaa catgcctggc cctcaacatc cgcaacaaag aattcaacta tcttcataat 180
 cgaaatgggt ctgaacttga ccttttgggg atgcgagatc tacttgaaaa ccttggatac 240
 tcagtgggta taaaagagaa tctcacagct caggaaatgg aaacagcact aaggcagttt 300
 gctgctcacc cagagcacca gtcctcagac agcacattcc tgggtgtttat gtcacatggc 360
 atcctgaatg gaatctgtgg gaccaagcac tgggatcaag agccagatgt tcttcacgat 420
 gacaccatct ttgaaatttt caacaaccgt aactgccaga gtctgaaaga caaacccaag 480
 gtcacatca tgcaagcctg ccgaggcaat ggtgctggga ttgtttgggt caccactgac 540
 agtgaaaaag ccagtgcaga tactcatggg cggctcttgc aaggtaacat ctgtaatgat 600
 gctgttacaa aggctcatgt ggaaaaggac ttcattgctt tcaaattctc cacaccacat 660
 aatgtttctt ggagacatga aacaaatggc tctgtcttca tttcccaaat tatctactac 720
 ttcagagagt attcttggag tcatcatcta gaggaattt ttcaaaagggt tcaacattca 780
 tttgagaccc caaatatact gaccagctg cccaccattg aaagactatc catgacacga 840
 tattttctatc tctttcttgg gaattaa 867

<210> 79
 <211> 288
 <212> PRT
 <213> Homo sapiens

<400> 79
 Ser Ala Leu Leu Glu Ile Gln Gly Ala Gln Pro Ser Gly Lys Leu Lys
 1 5 10 15
 Leu Cys Pro His Ala His Phe His Glu Leu Lys Thr Lys Arg Ala Asp
 20 25 30
 Glu Ile Tyr Pro Val Met Glu Lys Glu Arg Arg Thr Cys Leu Ala Leu
 35 40 45

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<210>      80
<211>      404
<212>      PRT
<213>      Homo Sapien

<400>      80
Met Ala Asp Lys Val Leu Lys Glu Lys Arg Lys Leu Phe Ile Arg Ser
1              5              10              15
Met Gly Glu Gly Thr Ile Asn Gly Leu Leu Asp Glu Leu Leu Gln Thr
              20              25              30
Arg Val Leu Asn Lys Glu Glu Met Glu Lys Val Lys Arg Glu Asn Ala
              35              40              45
Thr Val Met Asp Lys Thr Arg Ala Leu Ile Asp Ser Val Ile Pro Lys
              50              55              60

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Gly	Ala	Gln	Ala	Cys	Gln	Ile	Cys	Ile	Thr	Tyr	Ile	Cys	Glu	Glu	Asp	65	70	75	80
Ser	Tyr	Leu	Ala	Gly	Thr	Leu	Gly	Leu	Ser	Ala	Asp	Gln	Thr	Ser	Gly	85	90	95	
Asn	Tyr	Leu	Asn	Met	Gln	Asp	Ser	Gln	Gly	Val	Leu	Ser	Ser	Phe	Pro	100	105	110	
Ala	Pro	Gln	Ala	Val	Gln	Asp	Asn	Pro	Ala	Met	Pro	Thr	Ser	Ser	Gly	115	120	125	
Ser	Glu	Gly	Asn	Val	Lys	Leu	Cys	Ser	Leu	Glu	Glu	Ala	Gln	Arg	Ile	130	135	140	
Trp	Lys	Gln	Lys	Ser	Ala	Glu	Ile	Tyr	Pro	Ile	Met	Asp	Lys	Ser	Ser	145	150	155	160
Arg	Thr	Arg	Leu	Ala	Leu	Ile	Ile	Cys	Asn	Glu	Glu	Phe	Asp	Ser	Ile	165	170	175	
Pro	Arg	Arg	Thr	Gly	Ala	Glu	Val	Asp	Ile	Thr	Gly	Met	Thr	Met	Leu	180	185	190	
Leu	Gln	Asn	Leu	Gly	Tyr	Ser	Val	Asp	Val	Lys	Lys	Asn	Leu	Thr	Ala	195	200	205	
Ser	Asp	Met	Thr	Thr	Glu	Leu	Glu	Ala	Phe	Ala	His	Arg	Pro	Glu	His	210	215	220	
Lys	Thr	Ser	Asp	Ser	Thr	Phe	Leu	Val	Phe	Met	Ser	His	Gly	Ile	Arg	225	230	235	240
Glu	Gly	Ile	Cys	Gly	Lys	Lys	His	Ser	Glu	Gln	Val	Pro	Asp	Ile	Leu	245	250	255	
Gln	Leu	Asn	Ala	Ile	Phe	Asn	Met	Leu	Asn	Thr	Lys	Asn	Cys	Pro	Ser	260	265	270	
Leu	Lys	Asp	Lys	Pro	Lys	Val	Ile	Ile	Ile	Gln	Ala	Cys	Arg	Gly	Asp	275	280	285	
Ser	Pro	Gly	Val	Val	Trp	Phe	Lys	Asp	Ser	Val	Gly	Val	Ser	Gly	Asn	290	295	300	
Leu	Ser	Leu	Pro	Thr	Thr	Glu	Glu	Phe	Glu	Asp	Asp	Ala	Ile	Lys	Lys	305	310	315	320
Ala	His	Ile	Glu	Lys	Asp	Phe	Ile	Ala	Phe	Cys	Ser	Ser	Thr	Pro	Asp	325	330	335	
Asn	Val	Ser	Trp	Arg	His	Pro	Thr	Met	Gly	Ser	Val	Phe	Ile	Gly	Arg	340	345	350	
Leu	Ile	Glu	His	Met	Gln	Glu	Tyr	Ala	Cys	Ser	Cys	Asp	Val	Glu	Glu	355	360	365	
Ile	Phe	Arg	Lys	Val	Arg	Phe	Ser	Phe	Glu	Gln	Pro	Asp	Gly	Arg	Ala	370	375	380	
Gln	Met	Pro	Thr	Thr	Glu	Arg	Val	Thr	Leu	Thr	Arg	Cys	Phe	Tyr	Leu	385	390	395	400

Phe Pro Gly His

<210> 81
 <211> 377
 <212> PRT
 <213> Homo sapiens

<400> 81
 Met Ala Glu Asp Lys His Asn Lys Asn Pro Leu Lys Met Leu Glu Ser
 1 5 10 15
 Leu Gly Lys Glu Leu Ile Ser Gly Leu Leu Asp Asp Phe Val Glu Lys
 20 25 30
 Asn Val Leu Lys Leu Glu Glu Glu Glu Lys Lys Lys Ile Tyr Asp Ala
 35 40 45
 Lys Leu Gln Asp Lys Ala Arg Val Leu Val Asp Ser Ile Arg Gln Lys
 50 55 60
 Asn Gln Glu Ala Gly Gln Val Phe Val Gln Thr Phe Leu Asn Ile Asp
 65 70 75 80
 Lys Asn Ser Thr Ser Ile Lys Ala Pro Glu Thr Val Ala Gly Pro
 85 90 95
 Asp Glu Ser Val Gly Ser Ala Ala Thr Leu Lys Leu Cys Pro His Glu
 100 105 110
 Glu Phe Leu Lys Leu Cys Lys Glu Arg Ala Gly Glu Ile Tyr Pro Ile
 115 120 125
 Lys Glu Arg Lys Asp Arg Thr Arg Leu Ala Leu Ile Ile Cys Asn Thr
 130 135 140
 Glu Phe Asp His Met Pro Pro Arg Asn Gly Ala Ala Leu Asp Ile Leu
 145 150 155 160
 Gly Met Lys Gln Leu Leu Glu Gly Leu Gly Tyr Thr Val Glu Val Glu
 165 170 175
 Glu Lys Leu Thr Ala Arg Asp Met Glu Ser Val Leu Trp Lys Phe Ala
 180 185 190
 Ala Arg Glu Glu His Lys Ser Ser Asp Ser Thr Phe Leu Val Phe Met
 195 200 205
 Ser His Gly Ile Leu Asp Gly Ile Cys Gly Thr Met His Ser Glu Glu
 210 215 220
 Glu Pro Asp Val Leu Pro Tyr Asp Thr Ile Phe Arg Thr Phe Asn Asn
 225 230 235 240
 Arg Asn Cys Leu Ser Leu Lys Asp Lys Pro Lys Val Ile Ile Val Gln
 245 250 255
 Ala Cys Arg Gly Ala Asn Arg Gly Glu Leu Trp Val Ser Asp Ser Pro
 260 265 270
 Pro Ala Leu Ala Asp Ser Phe Ser Gln Ser Ser Glu Asn Leu Glu Glu
 275 280 285

Asp Ala Val Tyr Lys Thr His Val Glu Lys Asp Phe Ile Ala Phe Cys
290 295 300

Ser Ser Thr Pro His Asn Val Ser Trp Arg Asp Ile Lys Lys Gly Ser
305 310 315 320

Leu Phe Ile Thr Arg Leu Ile Thr Cys Phe Gln Lys Tyr Ala Trp Cys
325 330 335

Cys His Leu Glu Glu Val Phe Arg Lys Val Gln Gln Ser Phe Glu Lys
340 345 350

Pro Asn Val Lys Ala Gln Met Pro Thr Val Glu Arg Leu Ser Met Thr
355 360 365

Arg Tyr Phe Tyr Leu Phe Pro Gly Asn
370 375

<210> 82

<211> 377

<212> PRT

<213> Homo sapiens

<400> 82

Met Ala Glu Gly Asn His Arg Lys Lys Pro Leu Lys Val Leu Glu Ser
1 5 10 15

Leu Gly Lys Asp Phe Leu Thr Gly Val Leu Asp Asn Leu Val Glu Gln
20 25 30

Asn Val Leu Asn Trp Lys Glu Glu Glu Lys Lys Lys Tyr Tyr Asp Ala
35 40 45

Lys Thr Glu Asp Lys Val Arg Val Met Ala Asp Ser Met Gln Glu Lys
50 55 60

Gln Arg Met Ala Gly Gln Met Leu Leu Gln Thr Phe Phe Asn Ile Asp
65 70 75 80

Gln Ile Ser Pro Asn Lys Lys Ala His Pro Asn Met Glu Ala Gly Pro
85 90 95

Pro Glu Ser Gly Glu Ser Thr Asp Ala Leu Lys Leu Cys Pro His Glu
100 105 110

Glu Phe Leu Arg Leu Cys Lys Glu Arg Ala Glu Glu Ile Tyr Pro Ile
115 120 125

Lys Glu Arg Asn Asn Arg Thr Arg Leu Ala Leu Ile Ile Cys Asn Thr
130 135 140

Glu Phe Asp His Leu Pro Pro Arg Asn Gly Ala Asp Phe Asp Ile Thr
145 150 155 160

Gly Met Lys Glu Leu Leu Glu Gly Leu Asp Tyr Ser Val Asp Val Glu
165 170 175

Glu Asn Leu Thr Ala Arg Asp Met Glu Ser Ala Leu Arg Ala Phe Ala
180 185 190

Thr Arg Pro Glu His Lys Ser Ser Asp Ser Thr Phe Leu Val Leu Met
195 200 205

Ser His Gly Ile Leu Glu Gly Ile Cys Gly Thr Val His Asp Glu Lys
 210 215 220

Lys Pro Asp Val Leu Leu Tyr Asp Thr Ile Phe Gln Ile Phe Asn Asn
 225 230 235 240

Arg Asn Cys Leu Ser Leu Lys Asp Lys Pro Lys Val Ile Ile Val Gln
 245 250 255

Ala Cys Arg Gly Ala Asn Arg Gly Glu Leu Trp Val Arg Asp Ser Pro
 260 265 270

Ala Ser Leu Glu Val Ala Ser Ser Gln Ser Ser Glu Asn Leu Glu Glu
 275 280 285

Asp Ala Val Tyr Lys Thr His Val Glu Lys Asp Phe Ile Ala Phe Cys
 290 295 300

Ser Ser Thr Pro His Asn Val Ser Trp Arg Asp Ser Thr Met Gly Ser
 305 310 315 320

Ile Phe Ile Thr Gln Leu Ile Thr Cys Phe Gln Lys Tyr Ser Trp Cys
 325 330 335

Cys His Leu Glu Glu Val Phe Arg Lys Val Gln Gln Ser Phe Glu Thr
 340 345 350

Pro Arg Ala Lys Ala Gln Met Pro Thr Ile Glu Arg Leu Ser Met Thr
 355 360 365

Arg Tyr Phe Tyr Leu Phe Pro Gly Asn
 370 375

<210> 83
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 <212> PRT
 <213> Homo sapiens

<400> 83
 Met Phe Lys Gly Ile Leu Gln Ser Gly Leu Asp Asn Phe Val Ile Asn
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His Met Leu Lys Asn Asn Val Ala Gly Gln Thr Ser Ile Gln Thr Leu
 20 25 30

Val Pro Asn Thr Asp Gln Lys Ser Thr Ser Val Lys Lys Asp Asn His
 35 40 45

Lys Lys Lys Thr Val Lys Met Leu Glu Tyr Leu Gly Lys Asp Val Leu
 50 55 60

His Gly Val Phe Asn Tyr Leu Ala Lys His Asp Val Leu Thr Leu Lys
 65 70 75 80

Glu Glu Glu Lys Lys Lys Tyr Tyr Asp Ala Lys Ile Glu Asp Lys Ala
 85 90 95

Leu Ile Leu Val Asp Ser Leu Arg Lys Asn Arg Val Ala His Gln Met
 100 105 110

Phe Thr Gln Thr Leu Leu Asn Met Asp Gln Lys Ile Thr Ser Val Lys
 115 120 125

Pro Leu Leu Gln Ile Glu Ala Gly Pro Pro Glu Ser Ala Glu Ser Thr
130 135 140

Asn Ile Leu Lys Leu Cys Pro Arg Glu Glu Phe Leu Arg Leu Cys Lys
145 150 155 160

Lys Asn His Asp Glu Ile Tyr Pro Ile Lys Lys Arg Glu Asp Arg Arg
165 170 175

Arg Leu Ala Leu Ile Ile Cys Asn Thr Lys Phe Asp His Leu Pro Ala
180 185 190

Arg Asn Gly Ala His Tyr Asp Ile Val Gly Met Lys Arg Leu Leu Gln
195 200 205

Gly Leu Gly Tyr Thr Val Val Asp Glu Lys Asn Leu Thr Ala Arg Asp
210 215 220

Met Glu Ser Val Leu Arg Ala Phe Ala Ala Arg Pro Glu His Lys Ser
225 230 235 240

Ser Asp Ser Thr Phe Leu Val Leu Met Ser His Gly Ile Leu Glu Gly
245 250 255

Ile Cys Gly Thr Ala His Lys Lys Lys Lys Pro Asp Val Leu Leu Tyr
260 265 270

Asp Thr Ile Phe Gln Ile Phe Asn Asn Arg Asn Cys Leu Ser Leu Lys
275 280 285

Asp Lys Pro Lys Val Ile Ile Val Gln Ala Cys Arg Gly Glu Lys His
290 295 300

Gly Glu Leu Trp Val Arg Asp Ser Pro Ala Ser Leu Ala Val Ile Ser
305 310 315 320

Ser Gln Ser Ser Glu Asn Leu Glu Ala Asp Ser Val Cys Lys Ile His
325 330 335

Glu Glu Lys Asp Phe Ile Ala Phe Cys Ser Ser Thr Pro His Asn Val
340 345 350

Ser Trp Arg Asp Arg Thr Arg Gly Ser Ile Phe Ile Thr Glu Leu Ile
355 360 365

Thr Cys Phe Gln Lys Tyr Ser Cys Cys Cys His Leu Met Glu Ile Phe
370 375 380

Arg Lys Val Gln Lys Ser Phe Glu Val Pro Gln Ala Lys Ala Gln Met
385 390 395 400

Pro Thr Ile Glu Arg Ala Thr Leu Thr Arg Asp Phe Tyr Leu Phe Pro
405 410 415

Gly Asn

<210> 84
<211> 419
<212> PRT
<213> Mouse

<400> 84

Met	Ala	Ala	Arg	Arg	Thr	His	Glu	Arg	Asp	Pro	Ile	Tyr	Lys	Ile	Lys
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			20					25					30		
Lys	Asn	Val	Leu	Asn	Gly	Asp	Glu	Leu	Leu	Lys	Ile	Gly	Glu	Ser	Ala
		35					40					45			
Ser	Phe	Ile	Leu	Asn	Lys	Ala	Glu	Asn	Leu	Val	Glu	Asn	Phe	Leu	Glu
	50					55					60				
Lys	Thr	Asp	Met	Ala	Gly	Lys	Ile	Phe	Ala	Gly	His	Ile	Ala	Asn	Ser
65					70					75					80
Gln	Glu	Gln	Leu	Ser	Leu	Gln	Phe	Ser	Asn	Asp	Glu	Asp	Asp	Gly	Pro
				85					90					95	
Gln	Lys	Ile	Cys	Thr	Pro	Ser	Ser	Pro	Ser	Glu	Ser	Lys	Arg	Lys	Val
			100					105					110		
Glu	Asp	Asp	Glu	Met	Glu	Val	Asn	Ala	Gly	Leu	Ala	His	Glu	Ser	His
			115				120					125			
Leu	Met	Leu	Thr	Ala	Pro	His	Gly	Leu	Gln	Ser	Ser	Glu	Val	Gln	Asp
	130					135						140			
Thr	Leu	Lys	Leu	Cys	Pro	Arg	Asp	Gln	Phe	Cys	Lys	Ile	Lys	Thr	Glu
145					150					155					160
Arg	Ala	Lys	Glu	Ile	Tyr	Pro	Val	Met	Glu	Lys	Glu	Gly	Arg	Thr	Arg
				165					170					175	
Leu	Ala	Leu	Ile	Ile	Cys	Asn	Lys	Lys	Phe	Asp	Tyr	Leu	Phe	Asp	Arg
			180					185					190		
Asp	Asn	Ala	Asp	Thr	Asp	Ile	Leu	Asn	Met	Gln	Glu	Leu	Leu	Glu	Asn
		195					200					205			
Leu	Gly	Tyr	Ser	Val	Val	Leu	Lys	Glu	Asn	Leu	Thr	Ala	Gln	Glu	Met
	210					215					220				
Glu	Thr	Glu	Leu	Met	Gln	Phe	Ala	Gly	Arg	Pro	Glu	His	Gln	Ser	Ser
225					230					235					240
Asp	Ser	Thr	Phe	Leu	Val	Phe	Met	Ser	His	Gly	Ile	Leu	Glu	Gly	Ile
				245					250					255	
Cys	Gly	Val	Lys	His	Arg	Asn	Lys	Lys	Pro	Asp	Val	Leu	His	Asp	Asp
			260					265					270		
Thr	Ile	Phe	Lys	Ile	Phe	Asn	Asn	Ser	Asn	Cys	Arg	Ser	Leu	Arg	Asn
		275					280					285			
Lys	Pro	Lys	Ile	Leu	Ile	Met	Gln	Ala	Cys	Arg	Gly	Arg	Tyr	Asn	Gly
	290					295					300				
Thr	Ile	Trp	Val	Ser	Thr	Asn	Lys	Gly	Ile	Ala	Thr	Ala	Asp	Thr	Asp
305					310					315					320
Glu	Glu	Arg	Val	Leu	Ser	Cys	Lys	Trp	Asn	Asn	Ser	Ile	Thr	Lys	Ala

325 330 335

His Val Glu Thr Asp Phe Ile Ala Phe Lys Ser Ser Thr Pro His Asn
340 345 350

Ile Ser Trp Lys Val Gly Lys Thr Gly Ser Leu Phe Ile Ser Lys Leu
355 360 365

Ile Asp Cys Phe Lys Lys Tyr Cys Trp Cys Tyr His Leu Glu Glu Ile
370 375 380

Phe Arg Lys Val Gln His Ser Phe Glu Val Pro Gly Glu Leu Thr Gln
385 390 395 400

Met Pro Thr Ile Glu Arg Val Ser Met Thr Arg Tyr Phe Tyr Leu Phe
405 410 415

Pro Gly Asn

<210> 85
<211> 373
<212> PRT
<213> Mouse

<400> 85
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Leu Gly Lys Glu Val Leu Thr Glu Tyr Leu Glu Lys Leu Val Gln Ser
20 25 30

Asn Val Leu Lys Leu Lys Glu Glu Asp Lys Gln Lys Phe Asn Asn Ala
35 40 45

Glu Arg Ser Asp Lys Arg Trp Val Phe Val Asp Ala Met Lys Lys Lys
50 55 60

His Ser Lys Val Gly Glu Met Leu Leu Gln Thr Phe Phe Ser Val Asp
65 70 75 80

Pro Gly Ser His His Gly Glu Ala Asn Leu Glu Met Glu Glu Pro Glu
85 90 95

Glu Ser Leu Asn Thr Leu Lys Leu Cys Ser Pro Glu Glu Phe Thr Arg
100 105 110

Leu Cys Arg Glu Lys Thr Gln Glu Ile Tyr Pro Ile Lys Glu Ala Asn
115 120 125

Gly Arg Thr Arg Lys Ala Leu Ile Ile Cys Asn Thr Glu Phe Lys His
130 135 140

Leu Ser Leu Arg Tyr Gly Ala Lys Phe Asp Ile Ile Gly Met Lys Gly
145 150 155 160

Leu Leu Glu Asp Leu Gly Tyr Asp Val Val Lys Glu Glu Leu Thr
165 170 175

Ala Glu Gly Met Glu Ser Glu Met Lys Asp Phe Ala Ala Leu Ser Glu
180 185 190

His Gln Thr Ser Asp Ser Thr Phe Leu Val Leu Met Ser His Gly Thr

195	200	205
Leu His Gly Ile Cys Gly Thr Met His Ser Glu Lys Thr Pro Asp Val		
210	215	220
Leu Gln Tyr Asp Thr Ile Tyr Gln Ile Phe Asn Asn Cys His Cys Pro		
225	230	235
Gly Leu Arg Asp Lys Pro Lys Val Ile Ile Val Gln Ala Cys Arg Gly		
	245	250
Gly Asn Ser Gly Glu Met Trp Ile Arg Glu Ser Ser Lys Pro Gln Leu		
	260	265
Cys Arg Gly Val Asp Leu Pro Arg Asn Met Glu Ala Asp Ala Val Lys		
	275	280
Leu Ser His Val Glu Lys Asp Phe Ile Ala Phe Tyr Ser Thr Thr Pro		
	290	295
His His Leu Ser Tyr Arg Asp Lys Thr Gly Gly Ser Tyr Phe Ile Thr		
305	310	315
Arg Leu Ile Ser Cys Phe Arg Lys His Ala Cys Ser Cys His Leu Phe		
	325	330
Asp Ile Phe Leu Lys Val Gln Gln Ser Phe Glu Lys Ala Ser Ile His		
	340	345
Ser Gln Met Pro Thr Ile Asp Arg Ala Thr Leu Thr Arg Tyr Phe Tyr		
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Leu Phe Pro Gly Asn		
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29

<210> 87
 <211> 21
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<400> 87
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21

<210> 88
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 <212> DNA
 <213> Primer

<400> 88
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24

<210> 89
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<400> 89
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<210> 90
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<212> DNA
<213> Primer

<400> 90
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<210> 91
<211> 29
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<400> 91
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<210> 92
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<400> 92
cggatccctc agctcttctg gaaatccagg g 31

<210> 93
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<210> 95
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<400> 95
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<210> 96
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<400> 96
 cacggatccc gccgccatgg cagctcttc

29

<210> 97
 <211> 435
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<400> 97
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 Pro His His Gln Glu Thr Leu Lys Lys Asn Arg Val Val Leu Ala Lys
 20 25 30
 Gln Leu Leu Leu Ser Glu Leu Leu Glu His Leu Leu Glu Lys Asp Ile
 35 40 45
 Ile Thr Leu Glu Met Arg Glu Leu Ile Gln Ala Lys Val Gly Ser Phe
 50 55 60
 Ser Gln Asn Val Glu Leu Leu Asn Leu Leu Pro Lys Arg Gly Pro Gln
 65 70 75 80
 Ala Phe Asp Ala Phe Cys Glu Ala Leu Arg Glu Thr Lys Gln Gly His
 85 90 95
 Leu Glu Asp Met Leu Leu Thr Thr Leu Ser Gly Leu Gln His Val Leu
 100 105 110
 Pro Pro Leu Ser Cys Asp Tyr Asp Leu Ser Leu Pro Phe Pro Val Cys
 115 120 125
 Glu Ser Cys Pro Leu Tyr Lys Lys Leu Arg Leu Ser Thr Asp Thr Val
 130 135 140
 Glu His Ser Leu Asp Asn Lys Asp Gly Pro Val Cys Leu Gln Val Lys
 145 150 155 160
 Pro Cys Thr Pro Glu Phe Tyr Gln Thr His Phe Gln Leu Ala Tyr Arg
 165 170 175
 Leu Gln Ser Arg Pro Arg Gly Leu Ala Leu Val Leu Ser Asn Val His
 180 185 190
 Phe Thr Gly Glu Lys Glu Leu Glu Phe Arg Ser Gly Gly Asp Val Asp
 195 200 205
 His Ser Thr Leu Val Thr Leu Phe Lys Leu Leu Gly Tyr Asp Val His
 210 215 220
 Val Leu Cys Asp Gln Thr Ala Gln Glu Met Gln Glu Lys Leu Gln Asn
 225 230 235 240
 Phe Ala Gln Leu Pro Ala His Arg Val Thr Asp Ser Cys Ile Val Ala
 245 250 255

Val Glu Leu Met Arg Asp Val Ser Lys Glu Asp His Ser Lys Arg Ser
100 105 110

Ser Phe Val Cys Val Leu Leu Ser His Gly Glu Glu Gly Ile Ile Phe
115 120 125

Gly Thr Asn Gly Pro Val Asp Leu Lys Lys Ile Thr Asn Phe Phe Arg
130 135 140

Gly Asp Arg Cys Arg Ser Leu Thr Gly Lys Pro Lys Leu Phe Ile Ile
145 150 155 160

Gln Ala Cys Arg Gly Thr Glu Leu Asp Cys Gly Ile Glu Thr Asp Ser
165 170 175

Gly Val Asp Asp Asp Met Ala Cys His Lys Ile Pro Val Asp Ala Asp
180 185 190

Phe Leu Tyr Ala Tyr Ser Thr Ala Pro Gly Tyr Tyr Ser Trp Arg Asn
195 200 205

Ser Lys Asp Gly Ser Trp Phe Ile Gln Ser Leu Cys Ala Met Leu Lys
210 215 220

Gln Tyr Ala Asp Lys Leu Glu Phe Met His Ile Leu Thr Arg Val Asn
225 230 235 240

Arg Lys Val Ala Thr Glu Phe Glu Ser Phe Ser Phe Asp Ala Thr Phe
245 250 255

His Ala Lys Lys Gln Ile Pro Cys Ile Val Ser Met Leu Thr Lys Glu
260 265 270

Leu Tyr Phe Tyr His
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<210> 99

<211> 293

<212> PRT

<213> Homo sapiens

<400> 99

Met Ser Ser Ala Ser Gly Leu Arg Arg Gly His Pro Ala Gly Gly Glu
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Glu Asn Met Thr Glu Thr Asp Ala Phe Tyr Lys Arg Glu Met Phe Asp
20 25 30

Pro Ala Glu Lys Tyr Lys Met Asp His Arg Arg Arg Gly Ile Ala Leu
35 40 45

Ile Phe Asn His Glu Arg Phe Phe Trp His Leu Thr Leu Pro Glu Arg
50 55 60

Arg Arg Thr Cys Ala Asp Arg Asp Asn Leu Thr Arg Arg Phe Ser Asp
65 70 75 80

Leu Gly Phe Glu Val Lys Cys Phe Asn Asp Leu Lys Ala Glu Glu Leu
85 90 95

Leu Leu Lys Ile His Glu Val Ser Thr Val Ser His Ala Asp Ala Asp
100 105 110

Cys Phe Val Cys Val Phe Leu Ser His Gly Glu Gly Asn His Ile Tyr
115 120 125

Trp Leu Cys Phe Ser

Ala	Tyr	Asp	Ala	Lys	Ile	Glu	Ile	Gln	Thr	Leu	Thr	Gly	Leu	Phe	Lys
130						135				140					
Gly	Asp	Lys	Cys	His	Ser	Leu	Val	Gly	Lys	Pro	Lys	Ile	Phe	Ile	Ile
145					150					155					160
Gln	Ala	Cys	Arg	Gly	Asn	Gln	His	Asp	Val	Pro	Val	Ile	Pro	Leu	Asp
				165					170					175	
Val	Val	Asp	Asn	Gln	Thr	Glu	Lys	Leu	Asp	Thr	Asn	Ile	Thr	Glu	Val
			180					185					190		
Asp	Ala	Ala	Ser	Val	Tyr	Thr	Leu	Pro	Ala	Gly	Ala	Asp	Phe	Leu	Met
		195					200					205			
Cys	Tyr	Ser	Val	Ala	Glu	Gly	Tyr	Tyr	Ser	His	Arg	Glu	Thr	Val	Asn
	210					215					220				
Gly	Ser	Trp	Tyr	Ile	Gln	Asp	Leu	Cys	Glu	Met	Leu	Gly	Lys	Tyr	Gly
225					230					235					240
Ser	Ser	Leu	Glu	Phe	Thr	Glu	Leu	Leu	Thr	Leu	Val	Asn	Arg	Lys	Val
				245					250					255	
Ser	Gln	Arg	Arg	Val	Asp	Phe	Cys	Lys	Asp	Pro	Ser	Ala	Ile	Gly	Lys
			260					265					270		
Lys	Gln	Val	Pro	Cys	Phe	Ala	Ser	Met	Leu	Thr	Lys	Lys	Leu	His	Phe
	275						280					285			
Phe	Pro	Lys	Ser	Asn											
	290														
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<213>	Homo sapiens														
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Ala	Asn	Glu	Asp	Ser	Val	Asp	Ala	Lys	Pro	Asp	Arg	Ser	Ser	Phe	Val
			20					25					30		
Pro	Ser	Leu	Phe	Ser	Lys	Lys	Lys	Lys	Asn	Val	Thr	Met	Arg	Ser	Ile
		35					40					45			
Lys	Thr	Thr	Arg	Asp	Arg	Val	Pro	Thr	Tyr	Gln	Tyr	Asn	Met	Asn	Phe
	50					55					60				
Glu	Lys	Leu	Gly	Lys	Cys	Ile	Ile	Ile	Asn	Asn	Lys	Asn	Phe	Asp	Lys
65					70					75					80
Val	Thr	Gly	Met	Gly	Val	Arg	Asn	Gly	Thr	Asp	Lys	Asp	Ala	Glu	Ala
				85					90					95	
Leu	Phe	Lys	Cys	Phe	Arg	Ser	Leu	Gly	Phe	Asp	Val	Ile	Val	Tyr	Asn
			100					105					110		
Asp	Cys	Ser	Cys	Ala	Lys	Met	Gln	Asp	Leu	Leu	Lys	Lys	Ala	Ser	Glu
		115					120					125			

Pro Cys Val Val Ser Met Leu Thr Lys Glu Leu Tyr Phe Ser Gln
290 295 300

Ser Arg Ser Glu Leu Arg Ser Phe Lys Phe Leu Leu Gln Glu Glu Ile
115 120 125

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465 470 475

<210> 102
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<212> PRT
<213> Homo sapiens

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Glu Leu Phe Arg Pro His Met Ile Glu Asp Ile Gln Arg Ala Gly Ser
35 40 45
Gly Ser Arg Arg Asp Gln Ala Arg Gln Leu Ile Ile Asp Leu Glu Thr
50 55 60
Arg Gly Ser Gln Ala Leu Pro Leu Phe Ile Ser Cys Leu Glu Asp Thr
65 70 75 80
Gly Gln Asp Met Leu Ala Ser Phe Leu Arg Thr Asn Arg Gln Ala Ala
85 90 95
Lys Leu Ser Lys Pro Thr Leu Glu Asn Leu Thr Pro Val Val Leu Arg
100 105 110
Pro Glu Ile Arg Lys Pro Glu Val Leu Arg Pro Glu Thr Pro Arg Pro
115 120 125
Val Asp Ile Gly Ser Gly Gly Phe Gly Asp Val Gly Ala Leu Glu Ser
130 135 140
Leu Arg Gly Asn Ala Asp Leu Ala Tyr Ile Leu Ser Met Glu Pro Cys
145 150 155 160
Gly His Cys Leu Ile Ile Asn Asn Val Asn Phe Cys Arg Glu Ser Gly
165 170 175
Leu Arg Thr Arg Thr Gly Ser Asn Ile Asp Cys Glu Lys Leu Arg Arg
180 185 190
Arg Phe Ser Ser Pro His Phe Met Val Glu Val Lys Gly Asp Leu Thr
195 200 205
Ala Lys Lys Met Val Leu Ala Leu Leu Glu Leu Ala Gln Gln Asp His
210 215 220
Gly Ala Leu Asp Cys Cys Val Val Val Ile Leu Ser His Gly Cys Gln
225 230 235 240
Ala Ser His Leu Gln Phe Pro Gly Ala Val Tyr Gly Thr Asp Gly Cys
245 250 255
Pro Val Ser Val Glu Lys Ile Val Asn Ile Phe Asn Gly Thr Ser Cys
260 265 270
Pro Ser Leu Gly Gly Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Gly

275		280		285
Gly Glu Gln Lys Asp His Gly Phe Glu Val Ala Ser Thr Ser Pro Glu				
290		295		300
Asp Glu Ser Pro Gly Ser Asn Pro Glu Pro Asp Ala Thr Pro Phe Gln				
305		310		315
Glu Gly Leu Arg Thr Phe Asp Gln Leu Asp Ala Ile Ser Ser Leu Pro				
		325		330
Thr Pro Ser Asp Ile Phe Val Ser Tyr Ser Thr Phe Pro Gly Phe Val				
		340		345
Ser Trp Arg Asp Pro Lys Ser Gly Ser Trp Tyr Val Glu Thr Leu Asp				
		355		360
Asp Ile Phe Glu Gln Trp Ala His Ser Glu Asp Leu Gln Ser Leu Leu				
		370		375
Leu Arg Val Ala Asn Ala Val Ser Val Lys Gly Ile Tyr Lys Gln Met				
		385		390
Pro Gly Cys Phe Asn Phe Leu Arg Lys Lys Leu Phe Phe Lys Thr Ser				
		405		410
				415
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<211> 521				
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<213> Homo sapiens				
<400> 103				
Met Lys Ser Gln Gly Gln His Trp Tyr Ser Ser Ser Asp Lys Asn Cys				
1		5		10
Lys Val Ser Phe Arg Glu Lys Leu Leu Ile Ile Asp Ser Asn Leu Gly				
		20		25
Val Gln Asp Val Glu Asn Leu Lys Phe Leu Cys Ile Gly Leu Val Pro				
		35		40
Asn Lys Lys Leu Glu Lys Ser Ser Ser Ala Ser Asp Val Phe Glu His				
		50		55
Leu Leu Ala Glu Asp Leu Leu Ser Glu Glu Asp Pro Phe Phe Leu Ala				
		65		70
Glu Leu Leu Tyr Ile Ile Arg Gln Lys Lys Leu Leu Gln His Leu Asn				
		85		90
Cys Thr Lys Glu Glu Val Glu Arg Leu Leu Pro Thr Arg Gln Arg Val				
		100		105
Ser Leu Phe Arg Asn Leu Leu Tyr Glu Leu Ser Glu Gly Ile Asp Ser				
		115		120
Glu Asn Leu Lys Asp Met Ile Phe Leu Leu Lys Asp Ser Leu Pro Lys				
		130		135
Thr Glu Met Thr Ser Leu Ser Phe Leu Ala Phe Leu Glu Lys Gln Gly				
		145		150
Lys Ile Asp Glu Asp Asn Leu Thr Cys Leu Glu Asp Leu Cys Lys Thr				

				165					170					175			
Val	Val	Pro	Lys 180	Leu	Leu	Arg	Asn	Ile 185	Glu	Lys	Tyr	Lys	Arg 190	Glu	Lys		
Ala	Ile	Gln 195	Ile	Val	Thr	Pro	Pro 200	Val	Asp	Lys	Glu	Ala 205	Glu	Ser	Tyr		
Gln	Gly 210	Glu	Glu	Glu	Leu	Val 215	Ser	Gln	Thr	Asp	Val 220	Lys	Thr	Phe	Leu		
Glu 225	Ala	Leu	Pro	Gln	Glu 230	Ser	Trp	Gln	Asn	Lys 235	His	Ala	Gly	Ser	Asn 240		
Gly	Asn	Arg	Ala	Thr 245	Asn	Gly	Ala	Pro	Ser 250	Leu	Val	Ser	Arg	Gly 255	Met		
Gln	Gly	Ala	Ser 260	Ala	Asn	Thr	Leu	Asn 265	Ser	Glu	Thr	Ser	Thr 270	Lys	Arg		
Ala	Ala	Val 275	Tyr	Arg	Met	Asn	Arg 280	Asn	His	Arg	Gly	Leu 285	Cys	Val	Ile		
Val	Asn 290	Asn	His	Ser	Phe	Thr 295	Ser	Leu	Lys	Asp	Arg 300	Gln	Gly	Thr	His		
Lys 305	Asp	Ala	Glu	Ile	Leu 310	Ser	His	Val	Phe	Gln 315	Trp	Leu	Gly	Phe	Thr 320		
Val	His	Ile	His	Asn 325	Asn	Val	Thr	Lys	Val 330	Glu	Met	Glu	Met	Val 335	Leu		
Gln	Lys	Gln 340	Lys	Cys	Asn	Pro	Ala 345	His	Ala	Asp	Gly	Asp	Cys 350	Phe	Val		
Phe	Cys	Ile 355	Leu	Thr	His	Gly	Arg 360	Phe	Gly	Ala	Val	Tyr 365	Ser	Ser	Asp		
Glu 370	Ala	Leu	Ile	Pro	Ile	Arg 375	Glu	Ile	Met	Ser	His 380	Phe	Thr	Ala	Leu		
Gln 385	Cys	Pro	Arg	Leu	Ala 390	Glu	Lys	Pro	Lys	Leu 395	Phe	Phe	Ile	Gln	Ala 400		
Cys	Gln	Gly	Glu	Glu 405	Ile	Gln	Pro	Ser	Val 410	Ser	Ile	Glu	Ala	Asp 415	Ala		
Leu	Asn	Pro 420	Glu	Gln	Ala	Pro	Thr	Ser 425	Leu	Gln	Asp	Ser	Ile 430	Pro	Ala		
Glu	Ala	Asp 435	Phe	Leu	Leu	Gly	Leu 440	Ala	Thr	Val	Pro	Gly 445	Tyr	Val	Ser		
Phe 450	Arg	His	Val	Glu	Glu	Gly 455	Ser	Trp	Tyr	Ile	Gln 460	Ser	Leu	Cys	Asn		
His 465	Leu	Lys	Lys	Leu	Val 470	Pro	Arg	Met	Leu	Lys 475	Phe	Leu	Glu	Lys	Thr 480		
Met	Glu	Ile	Arg	Gly 485	Arg	Lys	Arg	Thr	Val 490	Trp	Gly	Ala	Lys	Gln 495	Ile		
Ser	Ala	Thr	Ser	Leu	Pro	Thr	Ala	Ile	Ser	Ala	Gln	Thr	Pro	Arg	Pro		

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Pro Met Arg Arg Trp Ser Ser Val Ser		
515	520	
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<211>	377	
<212>	PRT	
<213>	Homo sapiens	
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Met Ala Glu Asp Lys His Asn Lys Asn Pro Leu Lys Met Leu Glu Ser		
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Leu Gly Lys Glu Leu Ile Ser Gly Leu Leu Asp Asp Phe Val Glu Lys		
	20	25 30
Asn Val Leu Lys Leu Glu Glu Glu Lys Lys Lys Ile Tyr Asp Ala		
	35	40 45
Lys Leu Gln Asp Lys Ala Arg Val Leu Val Asp Ser Ile Arg Gln Lys		
	50	55 60
Asn Gln Glu Ala Gly Gln Val Phe Val Gln Thr Phe Leu Asn Ile Asp		
	65	70 75 80
Lys Asn Ser Thr Ser Ile Lys Ala Pro Glu Glu Thr Val Ala Gly Pro		
	85	90 95
Asp Glu Ser Val Gly Ser Ala Ala Thr Leu Lys Leu Cys Pro His Glu		
	100	105 110
Glu Phe Leu Lys Leu Cys Lys Glu Arg Ala Gly Glu Ile Tyr Pro Ile		
	115	120 125
Lys Glu Arg Lys Asp Arg Thr Arg Leu Ala Leu Ile Ile Cys Asn Thr		
	130	135 140
Glu Phe Asp His Met Pro Pro Arg Asn Gly Ala Ala Leu Asp Ile Leu		
	145	150 155 160
Gly Met Lys Gln Leu Glu Gly Leu Gly Tyr Thr Val Glu Val Glu		
	165	170 175
Glu Lys Leu Thr Ala Arg Asp Met Glu Ser Val Leu Trp Lys Phe Ala		
	180	185 190
Ala Arg Glu Glu His Lys Ser Ser Asp Ser Thr Phe Leu Val Phe Met		
	195	200 205
Ser His Gly Ile Leu Asp Gly Ile Cys Gly Thr Met His Ser Glu Glu		
	210	215 220
Glu Pro Asp Val Leu Pro Tyr Asp Thr Ile Phe Arg Thr Phe Asn Asn		
	225	230 235 240
Arg Asn Cys Leu Ser Leu Lys Asp Lys Pro Lys Val Ile Ile Val Gln		
	245	250 255
Ala Cys Arg Gly Ala Asn Arg Gly Glu Leu Trp Val Ser Asp Ser Pro		

				260					265					270			
Pro	Ala	Leu	Ala	Asp	Ser	Phe	Ser	Gln	Ser	Ser	Glu	Asn	Leu	Glu	Glu		
		275					280					285					
Asp	Ala	Val	Tyr	Lys	Thr	His	Val	Glu	Lys	Asp	Phe	Ile	Ala	Phe	Cys		
	290					295					300						
Ser	Ser	Thr	Pro	His	Asn	Val	Ser	Trp	Arg	Asp	Ile	Lys	Lys	Gly	Ser		
305					310					315					320		
Leu	Phe	Ile	Thr	Arg	Leu	Ile	Thr	Cys	Phe	Gln	Lys	Tyr	Ala	Trp	Cys		
				325					330					335			
Cys	His	Leu	Glu	Glu	Val	Phe	Arg	Lys	Val	Gln	Gln	Ser	Phe	Glu	Lys		
			340					345					350				
Pro	Asn	Val	Lys	Ala	Gln	Met	Pro	Thr	Val	Glu	Arg	Leu	Ser	Met	Thr		
		355					360					365					
Arg	Tyr	Phe	Tyr	Leu	Phe	Pro	Gly	Asn									
	370					375											
<210>	105																
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Met	Ser	Asn	Pro	Arg	Ser	Leu	Glu	Glu	Glu	Lys	Tyr	Asp	Met	Ser	Gly		
1				5					10					15			
Ala	Arg	Leu	Ala	Leu	Ile	Leu	Cys	Val	Thr	Lys	Ala	Arg	Glu	Gly	Ser		
			20					25					30				
Glu	Glu	Asp	Leu	Asp	Ala	Leu	Glu	His	Met	Phe	Arg	Gln	Leu	Arg	Phe		
		35					40					45					
Glu	Ser	Thr	Met	Lys	Arg	Asp	Pro	Thr	Ala	Glu	Gln	Phe	Gln	Glu	Glu		
	50					55					60						
Leu	Glu	Lys	Phe	Gln	Gln	Ala	Ile	Asp	Ser	Arg	Glu	Asp	Pro	Val	Ser		
65					70					75					80		
Cys	Ala	Phe	Val	Val	Leu	Met	Ala	His	Gly	Arg	Glu	Gly	Phe	Leu	Lys		
				85					90					95			
Gly	Glu	Asp	Gly	Glu	Met	Val	Lys	Leu	Glu	Asn	Leu	Phe	Glu	Ala	Leu		
			100					105					110				
Asn	Asn	Lys	Asn	Cys	Gln	Ala	Leu	Arg	Ala	Lys	Pro	Lys	Val	Tyr	Ile		
		115					120					125					
Ile	Gln	Ala	Cys	Arg	Gly	Glu	Gln	Arg	Asp	Pro	Gly	Glu	Thr	Val	Gly		
	130					135					140						
Gly	Asp	Glu	Ile	Val	Met	Val	Ile	Lys	Asp	Ser	Pro	Gln	Thr	Ile	Pro		
145					150					155					160		
Thr	Tyr	Thr	Asp	Ala	Leu	His	Val	Tyr	Ser	Thr	Val	Glu	Gly	Tyr	Ile		
				165					1								

Leu Gln

[illegible]